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parent, child, divisional, or issued patent numbers) along with i	e all pertinent information (	*For Sequence Searches Only. * Please includ	
		Earliest Priority Filing Date:	
		Inventors (please provide full names):	
		Title of Invention:	
уть, and registry numbers, and combine with the concept saning. Give examples or relevant citations, authors, etc, if abstract.	that may have a special me	mender the elected species of structures, at utility of the invention. Define any terms to known. Please attach a copy of the cover s	
as specifically as possible the subject matter to be searched	search topic, and describe	Please provide a detailed statement of the s	
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PTO-1590 (1-2000)

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	otein – protein search, using sw model	september 5, 2001, 10:54:03; Search time 21.04 Seconds (without alignments) 994.072 Million cell updates/sec	: US-09-457-066-43 St score: 1848 1 MILIGILITSALAGORIGTDVALEHHEECDCVCRGNAGG 345	ng table: BLOSUM62 Gapop 10.0 , Gapext 0.5	ned: 412676 segs, 60623988 residues	number of hits satisfying chosen parameters: 412676	um DB seq length: 0 um DB seq length: 2000000000	processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A_Geneseq_0601:*    SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseqp/AA1991.DAT:*   SIDS8/gcgdata/geneseqp/AA2001.DAT:*   SIDS8/gcgdata/geneseqp/geneseqp/AA2001.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*   SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*	
	OM protein -	Run on:	Title: Perfect score Sequence:	Scoring table	Searched:	Total number		Post-processing:	Database :	,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Docorintion	Description	Mouse zvegf3, SEQ	Murine vascular en	A murine platelet-	Human VEGF-E prote	Human PRO200 prote	Human vascular end	Human zveqf3, SEQ	Human platelet-der	Human PRO200 (UNQ1	Human RACE generat	Human VEGF-X prote
	1		AAB48658	AAY96861	AAY84559	AAY33679	AAY41766	AAY30023	AAB48657	AAB24250	AAB44322	AAB10633	AAB10635
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WPI; 2000-687541/67

Human VEGF-X prote	>	Human VEGF-X prote		Human PRO200 prote	Human PRO713 prote	Human TANGO 128.	Human growth facto	Bone morphogenic p	Human PRO200 prote	Human PRO200 prote	Human angiogenesis		Se	×	Human VEGF-X prote		Human VEGF-X prote	×	A fragment of plat	r a	Human VEGF-X prote	Bone morphogenic p	Murine TANGO 128.	Human growth facto	SEQ. ID. 37 from W	Human Platelet Der	Human VEGF-G prote	Human Platelet Der			×	Human VEGF-X CUB-1	Human VEGF-X PDGF-
AAB10644	AAB10650	AAB10651	AAB19578	AAB33414		AAB01419		AAY59285	AAB50980	AAB49895	AAB53074	AAB10639	AAY84557	AAB10634	AAB10636	AAB03003	AAB10640	AAB10641	AAY84558	AAB58438	AAB10653	AAY59286	AAB01427	AAB48653	AAY96864	AAY71130	AAB60888	AAY71129	AAB48663	AAB60895	AAB10652	AAB10643	AAB10642
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345	345	345	345	345	345	345	345	345	345	345	345	374	345	345	345	345	354	354	318	339	282	297	180	370	370	370	370	322	370	370	167	168	149
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12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; murine; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia; immunomodulation; hepatic. Gilbert T, Hart CE, Sheppard PO, Gilbertson DG; AAB48658 standard; Protein; 345 AA. 03-MAY-1999; 99US-0304216. 10-NOV-1999; 99US-0164463. 04-FEB-2000; 2000US-0180169. 03-MAY-2000; 2000WO-US40047. Mouse zvegf3, SEQ ID NO:35. 09-MAR-2001 (first entry) (ZYMO ) ZYMOGENETICS INC. WO200066736-A1. Mus musculus. 09-NOV-2000. AAB48658; RESULT AAB48658  ~

AAY96861;

useful

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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

CC of the PDGF (Platelet-derived growth factor)/FGGF (vascular endothelial

growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

CC AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like

CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like

CC CAAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like

CC CAAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like

CC Tragments thereof, and has also been shown to stimulate bone

CC Zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4/human zvegf4 human zvegf4 gene of a patient. Zvegf4 proteins and derived zvegf4 derived polypeptides; and a method of detecting a genetic zvegf4 derived polypeptides; and a method of detecting a genetic callular differentiation or proliferation. They are particularly used for the treatment of periodontal disease and fractures. They may also be used to multiple sclerosis). Due to their osteogenic activity, they may be used to multiple zelerosis). Due to their osteogenic and endothelial precursor stem cells, which may 
                                                                                                        for treating liver damage, ischemia, multiple sclerosis and
                                                                    Growth factor homologs and the nucleic acids that encode them,
                                                                                                                                                                                                    Disclosure; Page 130-131; 143pp; English
                                                                                                                                      Alzheimer's disease -
N-PSDB; AAC81583
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21; Length 345; Score 1848; DB 21; Pred. No. 2.3e-182; 0; Mismatches 0; 100.0%; Query Match 100. Best Local Similarity 100. Matches 345; Conservative 345 AA; Sequence

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Query Match 100.0%; Score 1848; DB 21; Length 345; Best Local Similarity 100.0%; Pred. No. 2.3e-182; Matches 345; Conservative 0; Mismatches 0; Indels 0;

345 AA;

Sequence

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nurine 2VEGT3 are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (b The "cysteine knot" structure of the platelet-derived growth factor of the "cysteine knot" structure of the platelet-derived growth factor (b The "cysteine knot" structure of the platelet-derived growth factor (b The "cysteine knot" structure of the platelet-derived growth factor (b The "cysteine knot" structure of the platelet-derived growth factor (b The "cysteine knot" structure of the platelet-derived growth factor (b The "cysteine knot" structural analysis and homology to CUB domains in neuropilins, human bone morphogenetic protein-", porcine seminal plasma tortein, bovine acidic seminal fluid protein and Xenopus laevis to the human zvegf3 gene has been mapped to chromosome 4Q28.3. ZVEGT3 is useful for stimulating the growth of fibroblasts or smooth muscles cells, for activating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for requilating (post-development) organ growth, regeneration and maintenance, as well as tissue maintenance and repair processes. ZVEGF3 diabetto retinopathy, ischemic lind disease, peripheral vascular intimal hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel gregf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising an epitope bearing portion of a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atheroscierosis, wound healing, chronic liver disease and haemangioma formation. ZVEGF3 can also be used to modulate neurite growth and development of the nervous system, and for treating neurodegenerative
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                                                                                                                              Vascular endothelial growth factor; homologue; zvegf3; CUB domain; Systeine Knot; platelet-derived growth factor; pDGF; neuropilin; chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker KE;
                                                                                    Murine vascular endothelial growth factor homologue, ZVEGF3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 169-170; 173pp; English:
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99US-0142576.
99US-0161653.
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                                         26-SEP-2000 (first entry)
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Gilbertson DG, West JW;
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N-PSDB; AAA51527.
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the PDGF-C
                                                                                                                                                                                                                                                                                                   growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents murine platelet-derived growth factor \langle ^{\rm PDGF-C} \rangle (formally designated VEGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation,
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                                  GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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        mll1g1111tsalaggrtgtraesnlssklqlssdkegngvqdprhervvtisgngsihs
                         PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                            LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYRPTWQLLGKAFLYGKKSKVVNLNL
×.
                                                                                                                                                                                                                                                                                            Platelet.derived growth factor C; PDGF-C; cell proliferation;
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                                                                                                                                                                        301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                              carcinoma; erythroleukemia; tissue remodelling
                                                                                                                                                                                                                                                                           A murine platelet-derived growth factor C (PDGF-C).
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Betsholz C;
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N-PSDB; AAA12525
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03-DEC-1998;
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and/or growth or motility of cells expressing a PDGF-C receptor. PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C. PDGF-C can also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                        and erythroleukemia, can be identífied by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population cells. Antagonists can also be used to treat fibrotic conditions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                especially found in the lung, kidney or liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 AA;
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301 vtkkyhevlqlrpktgvrglhksltdvalehheecdcvcrgstgg 345

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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquilizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially companies. It is useful in wound repair and tissue generation and create cardiac hypertrophy it can be combined with a carrier in pharmaceutical compositions, which can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to careen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or section therapeutically as antagonists, as above. The antibodies, useful therapeutically as antagonists, as above. The antibodies, useful therapeutically as antagonists, as above. The antibodies are also cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an antibody vEGF-E polypeptide complex. Polyucleotides encoding the antibody vEGF-E polypeptide complex. Polyucleotides encoding the antibody vEGF-E polypeptide complex. Polyucleotides encoding the antibody vEGF-E polypeptide complex. Polyucleotides encoding succeptibility to a disease related to a mutated form of vEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They may also be used to probes useful to detect related as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a samples. They may also be used to produce probes useful to detect related sequence isolated as a tumor of sequence or formation and per page to produce probes useful to detect related as sequence isolated as a tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New growth factor polypeptide useful for treating cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endothelial disorders, e.g. cardiac hypertrophy
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98US-0040220.
98US-0184216.
                                                                                                                                                                                      (GETH ) GENENTECH INC.
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17-MAR-1998;
02-NOV-1998;
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  Length 345;
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 DB 20;
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87.0%; Pred. No. 1.2e-163;
live 27; Mismatches 18;
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Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
      AAY41766 standard; Protein; 345 AA.
                                             Human PRO200 protein sequence.
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98US-0079786
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98US-0083392
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                                07-DEC-1999
                                                                                     Homo sapiens.
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29-APR-1998;
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                   AAY41766;
AAY41766
ID AAY4
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated tinclude blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted and transmembrane polypeptides and their polynucleotides,
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98US-0083495.
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29-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
05-MAY-1998;
06-MAY-1998;
07-MAY-1998;
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07-MAY-1998
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Chen J;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor related protein; VEGF-R protein; tissue growth inhibition; tumour growth; cancer; tissue growth; angiogenesis; coronary artery blockage.
PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFPSDGSVL
                                                                                                                                                                                                                                         GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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N-PSDB; AAX86352.
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                                                                                                                                                                                                                                                                                                                                                                 Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver dannage; neuroregenerative; Alicheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia;
                                                                                                                  180
                                                                                                                                                   240
                                                                                                                                                                                           240
                                                                                                                                                                                                           300
                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
                                                          Gaps
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                                                                          1 MILLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                  PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFPSDGSVL
                                                                                                                                         GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                          LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYRPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                   LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECOCVPRK
                                                                                                                                                                                                                   e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth factor homologs and the nucleic acids that encode them,
                                          Length 345;
                                                         Indels
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                                                                                                                                                                                                                                                   VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilbertson DG;
                                        90.2%; Score 1667; DB 20;
87.0%; Pred. No. 1.2e-163;
.ive 27; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheppard PO,
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                                                                                                                                                                                                                                                                                                  AAB48657 standard; Protein; 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0304216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2000; 2000WO-US40047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-1999; 99US-0164463
04-FEB-2000; 2000US-0180169
                                                                                                                                                                                                                                                                                                                                                  Human zvegf3, SEQ ID NO:33
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulation; hepatic
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hart CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-687541/67
  protein
                                                  Similarity
                  345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC81582
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200066736-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                  09-MAR-2001
                                                  Best Local Sim
Matches 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilbert T,
the VEGF-R
                                                                                                                                                                                                                                                                                                                  AAB48657;
                  Sequence
                                         Query Match
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The invention relates to the human growth factor homologue zvegf4

(AAB4865), and nucleic acids encoding it (AAC8155). Zvegf4 is a member

C of the PDGF (platelet-ted-troed growth factor)/VGGF (vascular endothelial

growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

CC (AAA9865) which has a beta barrel structure, and a CUB domain

CC (AAA9865) which has a beta barrel structure, vacqf4 has PDGF-like

CC (AAA9865) which has a beta barrel structure. Svegf4 has PDGF-like

CC (AAA9865) which has a beta barrel structure.

CC growth. The invention also relates to fusion proteins comprising human

C zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4

CC fusions; expression constructs and host cells comprising human zvegf4

CC nucleic acids; the recombinant expression of human zvegf4, an antibody

Which binds to human zvegf4 or a fragment thereof; a method of activating

CC cell-surface PDGF receptor using a zvegf4-derived polypeptide; a

CC method of modulating the proliferation, differentiation or

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic.

CC zvegf4-derived polypeptides; and a method of detecting a genetic of the treatment of perpen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human platelet-derived growth factor related protein LP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%; Score 1667; DB 21;
87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local Simi
Matches 300;
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AAB44322 standard; Protein; 345 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for enhancing tissue growth, promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LPB or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LPB antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LDB are useful for treating approaches. The present sequence represents human LPB, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 240
platelet derived growth factor related protein; LP8; VEGFh; ar endothelial growth factor h; tissue regeneration; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                         vascular endothelial growth factor h; tissue regeneration; vatherosclerosis; PDGF-related protein; antiarteriosclerotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.2%; Score 1667; DB 21;
87.0%; Pred. No. 1.2e-163;
Live 27; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 63-64; 64pp; English
                                                                                                                                                                                                                                                                                                                                    99US-0127913
                                                                                                                                                                                                                                                                           24-MAR-2000; 2000WO-US06427
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Best Local Similarity
Matches 300; Conserv
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                                                                                                                                                              WO200059940-A2
                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                 06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hammond LJ,
                                                                                                                                                                                                                       12-OCT-2000
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  Human;
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sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, eg. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
                                                                                                                                                                                                               protein; transmembrane protein; PRO; EST; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC78458 to AAC78599 represent polynucleotide and EST (expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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Gurney AL, Hillan KJ;
Paoni NF, Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eaton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 345;
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Wood WI:
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                                                                                                                                                          Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KP, Botstein D, Desnoyers L, E, Fong S, Gao W, Gerber H, PJ, Grimaldi CJ, Gurney AL, Napier MA, Pan J, Paon P, PA, FA, Tumas D, Williams PM, WC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the isolation of the PRO polynucleotide sequences.
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87.0%; Pred. No. 1.2e-163;
iive 27; Mismatches 18;
                                                                                                                                                                                                                                     expressed sequence tag; detection; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 207; 636pp; English.
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99US-0134287.
99US-0141037.
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99WO-US28551.
99WO-US28565.
99WO-US30095.
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99US-0126773
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                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara N, Filvaroff E, Goddard A, Godowski PJ, Kljavin IJ, Kuo SS, Nap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-611443/58.
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Best Local Similarity
Matches 300; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 AA;
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N-PSDB; AAC78582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization
                                                                                                 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFC1HYSIIMPQVTETTSPSVLPPSS 180
                                                                                                                                                           121 grwcgsgtvpgkqiskgnqirirfvsdeyfpsepgfcihynivmpqfteavspsvlppsa 180
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                                                           mslfglllltsalaggrqgtqaesnlsskfqfssnkeqngvqdpqheriitvstngsihs
                                                                                   PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
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99US-0124967.
99US-0164131.
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08-NOV-1999;
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regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the RACE generated human VEGF-X protein described in the method of the invention.
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87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
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18-MAR-1999;
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vascular endothelial growth factor; human; vulnerary; cytostatic;

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                                                                                                New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
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87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
                                Dijkmans JJH,
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                                You JR,
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                                Sprengel JJ,
           (JANC ) JANSSEN PHARM NV
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                                            Dhanaraj SN,
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                                Gordon RD,
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(first entry)

19-JAN-2001

Human VEGF-X protein #4

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(VEGF-X) protein (1a) and its encoding polynucleotide (1a) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidabetic activity and acts as an angiogenesis and vascularization certivity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic certinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ at subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein
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antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogeneeis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
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                                                                                                                            sore; diabetic ulcer; burns; skin graft growth.
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87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                          Homo sapiens
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Indels

Pred. No. 1.2e-163; 27; Mismatches

87.0%;

300; Conservative

Matches

Best Local Similarity

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This invention describes a novel vascular endothelial growth factor-X
(VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
vulnerary, cytostatic, antinhemmatic, antiantitic, antipsoriatic and
antidiabetic activity and acts as an angiogenesis and vascularization
regulator. An antisense molecule of the invention is useful for treating
or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
retinopathy by inhibiting angiogenic activity or inappropriate
vascularization including formation and proliferation of new blood
vessels, growth and development of tissues, tissue regeneration and organ
and tissue repair in a subject. The products of the invention are useful
for preparing medicaments for treating wounds such as dermal ulcers,
pressure sores, venous sores, diabetic ulcers and burns and to promote
tissue regeneration and organ repair, proliferation of new blood vessels,
tissue regeneration and organ repair by promoting angiogenic activity or
vascularization. This sequence represents the human 990126vegx protein
used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                   VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; antiologesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New vascular endothelial growth factor protein, useful for treating
 241 LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
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                                                               Dijkmans JJH,
                                                                                                                                                                                      AAB10650 standard; Protein; 345 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 11; 127pp; English.
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                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                       Human 990126vegx protein.
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08-NOV-1999;
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antirheumatic; antiarthritic; antiposofiatic; antidabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
                                                                                                                                                              240
                                                    61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFPSDGSVL 120
                                                                                                          121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
                                                                                                                         240
                                                                                                                                                                                                                   241 LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                                                                                                                                  9
              1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                                                                                                 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                                                                                                                                                                                                                                                                                                    AAB10651 standard; Protein; 345 AA.
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99US-0124967.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human VEGF-X protein #3.
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antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting anglogenic activity or vascularization. This sequence represents the human VEGF-X protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                         GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                              LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                    1 MLLLGLLLLTSALAGORTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                                                                                                                                                                                                                                                                                                             LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocular disease; retinopathy; maculopathy; therapy; retinits pigmentosa; macular degeneration; retinal detachment; retinal tear; macular hole; myopia; traumatic chorioretinopathy; acute retinal necrosis syndrome; contusion; edema; retinal vision occlusion; vascular disease; retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion.
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                                                                                                                                                                                         Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO200; vascular epithelial growth factor E; VEGF-E; human;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO200 (vascular endothelial growth factor E)
                                                                                                                                                                                        90.2%; Score 1667; DB 21;
87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signal_peptide
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/label= Mature_Pro200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB19578 standard; Protein; 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                  Best Local Similarity 87.0
Matches 300; Conservative
                                                                                                                                                        345 AA;
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                                                                                                                                                                                         Query Match
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The present sequence is that of human PRO200 or vascular endothelial growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515) that was isolated from a glioma cell line G61 ibrary using probes (see AAA88523-26) based on an expressed sequence tag (see AAA88522) that showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a pI of about 6.06. A method for producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal and photoreceptors and supportive cells displaced retinal and bignent epithelial cells) from injury and degradation. The retinal cells are preferably photoreceptors and photocreceptor cell injury or death is caused by retinal injury, light or environmental trauma or by an ocular disease selected from retinils pigmentosa, macular of degeneration, including age-related, retinal degenerative myopla, acute retinal necrosis syndrome, trainal cells, contained to the cells in the retinal necrosis syndrome, trainal cells, however, extinoned the contained to the cells of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kabakoff RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PRO polypeptides useful for preventing or rescuing retinal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                occlusion, collagen vascular diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and occlusion associated with Eales disease and systemic lupus erythematosus (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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87.0%; Pred. No. 1.2e-163;
tive 27; Mismatches 18;
                                    254..258
/note= "Asn is N-glycosylated"
/note= "Asn is N-glycosylated"
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Kuo SS, La Fleur M,
                                                                                                                                                                                /17...123
/note= "N-myristoylation"
127..133
/note= "N-myristoylation"
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282..288
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Kljavin IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
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Best Local Similarity
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A. Molecule type: DNA
A. Residues: 1-97 (HEL).
A. State in the control of the CYP21P pseudogene and CYP21 gene in a c
A. Note: an unequal cross-over mutation of the CYP21P pseudogene and CYP21 gene in a c
A. Rocession: S29672
A. Molecule type: DNA
A. Residues: 1-97 (HE2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cytochrome P450 21A/B mutant fusion protein - human NiAlternate names: steroid 21-monooxygenase C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) (C; Species: G5-Jan-1995 #sequence_revision 17-Aug-1995 #text_change 15-Feb-1996 C; Accession: S26485; S29672 R; Helmberg, A.; Kofler, R. Submitted to the EMBL Data Library, March 1991 A; Reference number: S26484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-494 cWHI.7
A;Cross-references: GB:M13936; NID:g187899; PIDN:AAA59695.1; PID:g386910
R;Higashi, Y.; Yoshioka, H.; Yamane, M.; Gotoh, O.; Fujii-Kuriyama, Y.
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100.0%; Pred. No. 0.3
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C;Genetics:
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Best Local Similarity 100.
Matches 9; Conservative
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C;Keywords: fusion protein
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N;Alternate names: cytochrome P450(GP-1)
C;Species: Cavia porcellus (guinea pig)
C;Jecies: Tavia porcellus (guinea pig)
C;Date: 31-Mar-1992 #sequence_revision 08-Peb-1996 #text_change 05-Mar-1999
C;Accession: S15135; S28205; A36154
R;Oguri, K.; Kaneko, H.; Tanimoto, Y.; Yamada, H.; Yoshimura, H.
Arch. Biochem. Biophys. 287, 105-111, 1991
A;Title: A constitutive form of guinea pig liver cytochrome P450 closely related to p A;Reference number: S15135; MUID:91378369
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A;Residues: 1-33 <ARC>
R;Yamada, H.; Kaneko, H.; Takeuchi, K.; Oguri, K.; Yoshimura, H.
Arch. Biochem. Biophys. 299, 248-254, 1992
A;Title: Tissue-specific expression, induction, and inhibition through metabolic inte
A;Reference number: S28205; MUID:93073973
                                                                                                                                                                                             Ricollier, S.; Tassabehji, M.; Strachan, T.
Nature Genet. 3, 260-255, 1993
Akittle: A de novo pathological point mutation at the 21-hydroxylase locus: implicati Akeference number: 159113; MUID:93251047
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A; Map position: 6p21.3-6p21.3
A; Introns: 67/1; 97/1; 148/3; 182/3; 245/3; 312/3; 372/2; 407/1
C; Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C; Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygena F; 288-450/Domain: cytochrome P450 homology <CYP>
F; 288-450/Domain: cytochrome P450 homology <CYP>
F; 428/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A;Title: Purification of a cytochrome P450 isozyme belonging to a subfamily of P450 I A;Reference number: A36154; MUID:91054472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CYP2B
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Reywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreduc
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 109-171, NV,173-185 <RE3>
A;Cross-references: GB:S60612; NID:9300314
C;Comment: Deficiency of this enzyme (21-hydroxylase deficiency) causes about 90
                                                                                     A;Residues: 149-182 <RE2>
A;Cross-references: GB:M19711; NID:g181289; PIDN:AAA83248.1; PID:g181290
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Best Local Similarity 100.9
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Best Local Similarity 100.
Matches 8; Conservative
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A;Molecule type: protein
A;Residues: 1-31 <YAM>
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Proc. Natl. Acad. Sci. U.S.A. 83, 2841-2845, 1986

A.Title: Complete nucleotide sequence of two steroid 21-hydroxylase genes tandemly arran A; Reference number: A00191; MUID: 86206051

A; Recession: A00191

A; Molecule type: mRNA
A; Residues: 1-425, FP, 427-494 (HIG>
B; Rodrigues, N.R.; Dunham, I: Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Campbell, R.D.
B; Rodrigues, N.R.; Dunham, I: Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Campbell, R.D.
R; Rodrigues, N.R.; Dunham, I: Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Campbell, R.D.
A; Residues: 10-425, FP, 427-494 (HIG>
A; Reference number: A27865; MUID: 8727858
A; Residues: 10-42, FY 10-101, R.Y., 103-372, S.Y.; 373-494 (ROD>
A; Residues: 10-5, FY, 10-101, R.Y., 103-372, S.Y.; 373-494 (ROD>
B; Matteson, R.J.; Phillips III, J.A.; Miller, W.L.; Chung, B.; Orlando, P.J.; Frisch, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 5858-5862, 1987
A; Title: A450XXI (steroid 21-hydroxylase) gene deletions are not found in family studies
A; Reference number: A32715; MUID: 87289701
A; Residues: 265-310, 'I', 312-345, 'I', 347-494 (KMI)
A; Residues: 265-310, 'I', Siller, RNA
A; Residues: 265-310, 'I', Siller, Porter, R.R.
B; Carroll, M.C.; Campbell, R.D.; Porter, R.R.
B; Roc. Natl. Acad. Sci. U.S.A. 82, 521-525, 1985
A; Title: Mapping of steroid 21-hydroxylase genes adjacent to complement component C4 gen
A; Reference number: ANB
A; Residues: 205-310, 'I', 312-345, 'I', 312-345, 'I', 312-345, 'I', 312-345, 'I', 312-345, 'I', 347-349, *ANB
A; Residues: 265-310, 'I', 347-349, *ANB
A; Russidues: 265-
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A;Molecule type: DNA
A;Residues: 1-9, TL',10-280, TL',282-494 <RES>
B;Anors, M.; Parker, K.L.; Globerman, H.; New, M.I.; White, P.C.
Proc. Natl. Acad. Sci. U.S.A. 85, 1600-1604, 1988
A;Title: Mutation in the CYP21B gene (Ile-172---Asn) causes steroid 21-hydroxylase defi
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A; Molecule type: DNA
A; Residues: 1-9,'L',10-101,'R',103-371 <HE4>
A; Cross-references: EMBL:X58902; NID:930325; PIDN:CAA41706.1; PID:930326
B; Helmberg, A.; Tabarelli, M.; Dobler, G.; Kofler, R.
Bibmitted to the EMBL Data Library, March 1991
A; Description: Identification of molecular defects causing congenital adrenal Hyperplasi
A; Reference number: S26584
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A; Molecule type: DNA
A; Residues: 149-171, NV, 173-182 <CAR>
A; Cassarreferences: GB: K02771; NID: g187928; PIDN: AAA59706.1; PID: g443672
R; Helmberg, A.; Kofler, R.
submitted to the EMBL Data Library, March 1991
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A.Molecule type: DNA
A.Molecule type: DNB
A.Molecule
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A;Cross-references: EMEL:X58904; NID:g30319; PIDN:CAA41707.1; PID:g30320
A;Accession: S29670
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A; Residues: 1-9, L', 10-101, R', 103-338, 'H', 340-452,'S', 454-492,'S', 494 < A; Cross-references: EMBL:X58906; NID:g30321; PIDN:CAA41709.1; PID:g30322
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: 159109
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C;Species: Vibrio cholerae
C;Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82294
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
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A; Estiduce: 1-130 (LEV)
A; Experimental source: follicular lymphoma cells
A; Experimental source: follicular lymphoma cells
A; Experimental source: shown here is derived from the consensus nucleotide sequence of
b; Note: the sequence shown here is derived from the consensus nucleotide sequence of
c; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; hybridoma; immunoglobulin
C; Keywords: heterotetramer; hybridoma; immunoglobulin
C; Keywords: netrotetramer; hybridoma; immunoglobulin
F; 33-130/Product: Ig kappa chain V-I region CJ #status predicted <MAT>
F; 38-112/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 168, 475-489, 1988
A;Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.
A;Reference number: S04936; MUID:88316166
A;Title: Mutational hot spots in Ig V region genes of human follicular lymphomds
A;Reference number: S04936; MUID:88316166
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: PL0113
                                                                                                            A.Molecule type: mRNA
A.Residues: 1-125 <LEV>
A.Residues: 1-125 <LEV>
A.Residues: 1-125 <LEV>
A.Cross-references: EMBL:X13076, NID:933173; PIDN:CAA31477.1; PID:9736243
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-125/Product: Iq kappa chain (fragment) #status predicted <MAT>
F:33-107/Domain: immunoglobulin homology <IMM>
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100.0%; Pred. No. 3.2
Live 0; Mismatches
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F;72-78/Region: complementarity-determining 2
F;111-130/Region: complementarity-determining 3
F;118-130/Region: JI
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100.0%; Pred. No. 3.3
:ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conserv
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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus and Rattus Ratt
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R;Ravanat, C.; Gachet, C.; Herbert, J.M.; Schuhler, S.; Guillemot, J.C.; Uzabiaga, F.; F
Biochem. 223, 203-210, 1994
A;Title: Rat platelets contain glycosylated and non-glycosylated forms of platelet factc
A;Reference number: 845657; MUID:94307262
A;Accession: S45657
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epididymis-specific four-disulfide core protein CE4 - dog
cyspecies: Canis lupus familiaris (dog)
Cyspecies: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 24-Oct-2000
CyAccession: 154768
CyRillerbrock, K.; Pera, I.; Hartung, S.; Ivell, R.
Int. J. Androl. 17, 314-323, 1994
Artile: Gene expression in the dog epididymis: a model for human epididymal function.
A) Reference number: 154768; MUID:95263175
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C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology
F;76-123/Domain: antileukoproteinase repeat homology <ALP>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 3.1
ive 0; Mismatches
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Pred. No.
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100.0%; Pre
0;
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A;Residues: 30-42 <RAV>
C;Superfamily: beta-thromboglobulin
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Best Local Similarity luu...
"~~ 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-105 <DOI>
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11 LLLGLLL 18
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LLLGLLLL 20
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A Status: preliminary
A; Molecule type: DNA
A; Residues: 1-380 <STO>
A; Cross-references: GB: AE004579; GB: AE004091; NID: g9947455; PIDN: AAG04898.1; GSPDB:GN
A; Experimental source: strain PAO1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA_A;Residues: 1-461 <HEI>A;Residues: 1-461 <HEI>A;Cross-references: GB:AE004206; GB:AE003852; NID:g9655749; PIDN:AAF94424.1; GSPDB:GNA;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: A83458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A82220
hypothetical protein VC1265 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C; Specias: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: A82220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R. Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833
A;Accession: A82220
                                                                                                                                                     C;Accession: A83458
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ...; Olson, M.V.
Nature 406, 959-964, 2000
                                      RESULT 11
A83458
hypothetical protein PA1509 [imported] - Pseudomonas aeruginosa (strain PA01)
C; Species: Pseudomonas aeruginosa
C; Species: Dseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3%; Score 8; DB 3100.0%; Pred. No. 8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches, 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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A;Gene: VC1265
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A;Residues: 1-221 <hEz>
A;Cross-references: GB:AE004153; GB:AE003852; NID:g9655103; PIDN:AAF93833.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetico: UC0668
A;Map position: 1
C;Superfamily: mutator mutH
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S43455
S43455
S43455
S52455
S5256258: Pichia angusta
C;Species: Pichia angusta
C;Species: Pichia angusta
C;Date: 13-Jan-1995 #sequence_revision 23-Feb-1996 #text_change 20-Apr-2000
C;Accession: S43459
SF349aphonov, M.O.; Poznyakovski, A.I.; Bogdanova, A.I.; Ter-Avanesyan, M.D.
S757176: ISOJAtion and characterization of the LEU2 gene of Hansenula polymorpha.
A;Reference number: S43454; MUID:95028149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribonuclease S homolog - maize
N;Alternate names: S-like RNase
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Char, B.R.; Hake, S.
Submitted to the EMBL Data Library, August 1996
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A;Cross-references: EMBL:U00889; NID:g392892; PIDN:AAA19110.1; PID:g392894
C;Genetics:
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A;Accession: T04095
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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5.8;
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Best Local Similarity 100.0%; Pred. No. 5.1
Matches 8; Conservative 0; Mismatches
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100.0%; Pred. No. 8;
ive 0; Mismatches
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Pred. No.
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100.0%; Pred
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
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FRESULT 13
Pypothetical protein - Deinococcus radiodurans (strain R1)
hypothetical protein - Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75257
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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      Length 461;
DB 2;
2.3%; Score 8; DB 2
100.0%; Pred. No. 9.6
tive 0; Mismatches
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197 EELIRYLE 204
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G86587
heat shock protein-60 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae 23-Mar-2001
C;Accession: G86587
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Reference number: A86491; MUID:20330349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-526 < STO>
A;Cross-references: GB:BA000008; NID:g8979150; PIDN:BAA989985.1; GSPDB:GN00142
C;Genetics: Strain J138
C;Genetics: Genetics: Strain J138
C;Superfamily: Chaperonin groEL
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Cispecies: D72036
Cispecies: D72036
A. Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A. Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A. Reference number: A72000; MUID:99206606
A. Reference number: A72000; MUID:99206606
A. Status: preliminary
A. Molecule 'type: DNA
A. Residues: 1-526 <ARN>
A. Residues: 1-526 <ARN>
A. Residues: 1-526 <ARN>
A. Residues: 1-526 <ARN>
A. Coss-references: GB:AE001659; GB:AE001363; NID:9437708]
Cigenetics: Strain CWL029
Cigenetics: Cigenetics: Chaperonin groEL
Cisperfamily: chaperonin groEL
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: F75257
A;Status: preliminary
A;Molecule: type: DNA
A;Residues: 1-496 < AMII>
A;Residues: 1-496 < AMII>
A;Cross-references: GB:AEC02086; GB:AEC00513; NID:g6460395; PIDN:AAF12116.1; PID:g64604C
C;Genetics:
C;Genetics:
A;Gene: DR2572
A;Map position: 1
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D72036
heat shock protein-60 - Chlamydophila pneumoniae (strain CWL029)
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100.0%; Pred. No. 11;
ative 0; Mismatches
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100.0%; Pred. No. 10;
... 0; Mismatches
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Best Local Similarity اللاب
الابتارية 8; Conservative
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        DB 2;
       Score 8; DB 2;
; Pred. No. 11;
0; Mismatches
2.3%; Scor.
100.0%; Pre
0; '
       Query Match 2.3
Best Local Similarity 100.
Matches 8; Conservative
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Gaps

Search completed: September 5, 2001, 10:57:14 Job time: 116 sec

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Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 6 Sequence 2 Sequence 2 Sequence 3 Sequence 3

Sequence Sequence Sequence

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APPLICANT: Brenner, Mitch
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 181; DB 1; Length 788;
42.6%; Pred. No. 6.7e-11;
tive 16; Mismatches 38; Indels
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APPLICATION NUMBER: US/08/572,225
FILING DATE: 13-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT TAXABLE
US-08-795-430-11
US-08-024-868-2
US-08-242-097-2
US-09-206-695-2
PCT-US96-11995-1
US-08-42-097-6
US-09-042-105-2
US-09-042-105-2
US-09-042-105-18
US-08-795-430-8
US-08-795-430-8
US-08-795-430-13
US-08-795-430-13
US-08-795-430-13
US-08-795-430-13
US-08-795-430-13
US-08-103-137-127
US-08-103-137-127
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NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-360
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/085722255; Patent No. 5807981
                                                                                                                                                                                                                                                                                                                                                 Prockop, Darwin J.
Hojima, Yoshio
Li, Shi-Wu
Sieron, Aleksander
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 42.6
Matches 46; Conservative
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; MOLECULE TYPE: protein
US-08-572-225-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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   APPLICANT: LAPPLICANT: SAPPLICANT: B
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APPLICANT:
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117.5
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128
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127.5
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   ; Search time 12.27 Seconds (without alignments) 578.946 Million cell updates/sec
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                                                                                                                                     US-09-457-066-43
1848
1 MLLIGLILITSALAGQRTGT......DVALEHHEECDCVCRGNAGG 345
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Sequence 5,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-021-287-3
US-08-991-08-4
US-08-91-408-4
US-08-01-287-5
US-08-839-008-2
US-08-839-008-2
US-08-839-008-3
US-08-936-135-24
US-08-936-135-24
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US-08-936-135-16
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US-08-915-795-3
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US-08-839-008-7
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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US-09-021-287-3
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55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                       62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
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                                                                                                       114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
9.1%; Score 169; DB 3;
Best Local Similarity 31.5%; Pred. No. 1.8e-09;
Matches 56; Conservative 21; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                       E: SCIENCE & TECHNOLOGY LAW GROUP 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                   APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
WUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GRC
                                                                                                                                                                                                                        Sequence 6, Application US/08936135 Patent No. 6054293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENY INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/POCKET NUMBER: 0097
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 75 DENACE CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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US-08-936-135-6
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US-08-866-650-3
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; Sequence 3, Application US/08866650

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55 NGSIHSPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-EE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             682 PSSESKLHGKFCGA-DIPEVMTSHFNNMRIEFKSDNTV-SKKGFKAHF 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Grachaspan, Razuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
APPLICANT: Greenspan, Daniel S
APPLICANT: Greenspan, Kazuhiko
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.9%; Score 165; DB 2;
Best Local Similarity 40.7%; Pred. No. 5.8e-09;
Matches 44; Conservative 21; Mismatches 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/866,650
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Quarles & Brady
1 South Pinckney Street
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Patent No. 5981717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514
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                                                                                                                                                                                                    CITY: Madison
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                                                                                                                                                                                                                                                                     ZIP: 53703
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204 NGTITTPGWPKEYPPNKNCVWQVVAPTQ-YRISVKF-EFFELG--NEVCKYDYVEIWSG 259
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                                                                                                                                                                                                                                                                                       Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 LSSESKLHGKFCGA-EVPEVITSQFNNMRIEFKSDNTV-SKKGFKAHF 305
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
VIMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUCRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
                                                                                                                                                                                                                                                                                 8.8%; Score 162; DB 3;
ilarity 39.8%; Pred. No. 5.2e-09;
Conservative 22; Mismatches 35,
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39.8%; Pred. No. 1.2e-08;
tive 22; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Berson, Bennett J
REGISTRATION VUNBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
    610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1013 amino acids
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Best Local Similarity 39.8°
Matches 43; Conservative
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                          610-407-0701
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-991-408-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-866-650-5
                                                                                                                                                                              linear
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3Y: linear
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Greensp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Madison
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      TELEPHONE:
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                        TELEFAX:
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US-08-866-650-5
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626 NGTITTPGWPKEYPPNKNCYMOVIAPSQ-YRISVKF-EFFELEG--NEVCKYDYVEIWSG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 PSDGSVL-GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ARETH, ANTHONY J.
APPLICANT: MILLETTE, ROBERT N.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
TITLE OF INVENTION: POTEIN
TUTLE OF INVENTION: POTEIN
TUTLE OF INVENTION: POTEIN
TUTLE OF LOUGHCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATHER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.9%; Score 165; DB 2; Best Local Similarity 40.7%; Pred. No. 5.8e-09; Matches 44; Conservative 21; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                              NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: ATG-50038 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,408
FILING DATE:
                                            APPLICATION NUMBER: US/09/021,287
                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/034,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08991408
Patent No. 6008017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1013 amino acids
                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-021-287-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19482
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113 8; 35; Indels

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APPLICANT: ELSHOURBAGY, NABIL A.
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Patent No. 5916758
                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hurle, Mark R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 846169
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.8
Best Local Similarity 39.8
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 1013 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 709 Sweeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-991-408-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                COUNTRY:
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55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1013;
                                                         114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                               114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
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Patent No. 5981717

GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/021,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.8%; Score 162; DB 2; Best Local Similarity 39.8%; Pred. No. 1.2e-08; Matches 43; Conservative 22; Mismatches 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
OB/866,650
FILING DATE:
ATOWNEY/AGENT INFORMATION:
NAME: BETSON, Bennett J
REGISTRATION NUMBER: 37094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08991408
Patent No. 6008017
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILLETTE, ROBERT N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARLETH, ANTHONY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-021-287-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              53703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                      RESULT 7
US-09-021-287-5
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US-08-991-408-2
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55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEF- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McDonnell, Peter C
APPLICANT: McNulty, Dean E
APPLICANT: Rosen, Craig A
APPLICANT: Siemens, Ivo R
APPLICANT: Young, Peter R
APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.8%; Score 162; DB 3; Length 1013;
39.8%; Pred. No. 1.2e-08;
tive 22; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/ns...
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: SmithKline Beecham Corporation
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/034,471
FILING DATE: 02-JAN-1997
ATTORNEY/AGBNT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
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56 GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 449;
                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.5%; Score 158; DB 2; Best Local Similarity 34.5%; Pred. No. 9.3e-09; Matches 48; Conservative 21; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08936135
Patent No. 6054293
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UC97-288-2
                           23.APR-1997
23.APR-1997
20.8
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PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    08/563,697
                                                                             FILING DATE: 23-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/563,69
RICHEN BAUME: 28-NOV-1995
ATORNEY/AGENT INFORMATION:
NAME: BAUMEISTER, XINK
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P503;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filing CLASSIFICATION: 455
CLASSIFICATION: 455
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
TINNER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 -- POVTETTSPSV-LPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 OGPGPKRGTEPKVKLPPKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 449 amino acids TYPE: amino acid
                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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US-08-936-135-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smooth Muscle Cell-Derived Migration Factor
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                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hurle, Mark R
APPLICANT: Horle, Mark R
APPLICANT: McDonnell, Peter C
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Stemens, Ivo R
APPLICANT: Young, Peter R
APPLICANT: Young, Peter R
APPLICANT: Young, Peter R
APPLICANT: Young, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derive, NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/563,697
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50384
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,008
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08839008
Patent No. 5916758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 QGPGPKRGTEPKVKLPPKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 -- POVTETTSPSV-LPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO: 2:
                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
STATE: P. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-839-008-9
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US-08-936-135-8
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                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                               34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                    16 SGHEVRSQODPPCGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                                 Length 901;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                               tch 8.4%; Score 155.5; DB 3; al Similarity 32.8%; Pred. No. 5.3e-08; 43; Conservative 18; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/08936135 Patent No. 6054293 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
                        TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEO ID NO: 24
SEQUENCE CHARACTERISTICS:
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 901 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                906 amino acids
                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-936-135-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 SEPGFCIHYSI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 OGAGESLRYEI 141
                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94010
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                                                                                                                                                                                                                                                                 Query Match
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76 FEIEKHD---CKYDFIEIRDGDSESADLLGKHCGN-IAPPTIISSGSVLYIKFTSD-YAR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 FGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 151
                                                                                                                            34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
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    Length 906;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 8.4%; Score 155.5; DB 3; Best Local Similarity 32.8%; Pred. No. 5.4e-08;
8.4%; Score 155.5; DB 3
32.8%; Pred. No. 5.4e-08;
tive 18; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: SCIENCE, & TECHNOLOGY LAW GROUP 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08936135
Patent No. 6054293
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPHAX: (650) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      909 amino acids
                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-936-135-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                            152 SEPGFCIHYSI 162
                                                                                                                                                                                                                                                                                                                                           131 QGAGFSLRYEI 141
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  Query Match
Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
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Search completed: September 5, 2001, 10:54:52
Job time: 49 sec
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 SGHEVRSQQDPPCGGRPNSKDAGXITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLIFDER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4%; Score 155.5; DB 3;
32.8%; Pred. No. 5.4e-08;
tive 18; Mismatches 63;
                                                                                                                                                                                   APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhiqang
APPLICANT: Chen, Hang
APPLICANT: Chen, Hang
APPLICANT: Chen, Hang
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tessier-Lavigne, Marc APPLICANT: He, Zhigang APPLICANT: Chen, Hang TITLE OF INVENTION: Semaphorin Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        Sequence 10, Application US/08936135 Patent No. 6054293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08936135 Patent No. 6054293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 56,627
REFERENCE/POCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 909 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.4%
Best Local Similarity 32.8%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-936-135-10
                                                                                                                                                                                                                                                                                                                                                           CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 SEPGFCIHYSI 162
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                 131 OGAGFSLRYEI 141
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                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-936-135-18
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94 FGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 909;
                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.4%; Score 155.5; DB 3 32.1%; Pred. No. 5.4e-08; tive 20; Mismatches 62
              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UC97-288-2
TELECOMMUNICATION INFORMATION:
TELEPHORE: (650) 343-4341
TELEPHORE: (650) 343-434
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 909 amino acids TYPE: amino acid . STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32.19
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide US-08-936-135-18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 SEPGFCIHYSI 162
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|131 QGAGFSLRYEI 141
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                                                                                                                                   94010
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

5, 2001, 10:54:03 September Run on:

; Search time 16.06 Seconds (without alignments) 1636.377 Million cell updates/sec

Perfect score:

US-09-457-066-43
1848
1 MLLGLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345 Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241

219241 seqs, 76174552 residues

Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

		d			SUMMARIES	
Result	Score	Query Match	Length	DB	Ţ	Description
	191	10.3	707	٠	TC2218	Opas Dager [Occur
1 7	190	10.3	823	٦,	A58788	י כ
ım	183.5	6.6	730	· ~	BMHU1	Ų
4	183.5	6.6	927	1	JQ0948	A5 antigen precurs
2	181		986	Н	B58788	procollagen C-endo
9	181	9.8	991	~	I49540	procollagen C-endo
7	174.5	9.4	3623	7	T09456	intrinsic factor-B
80	160	٠.	3623	7	T08618	intrinsic factor-B
6	158	8.5	449	~	A55362	procollagen I C-pr
10	153	٠,	1057	7	A39288	dorsal-ventral pat
11	147.5		1524	~	T30337	4
12	145.5	٠	989	٦	A59271	Ra-reactive factor
13	4	7.8	669	Н	154763	Ra-reactive factor
14	143.5		597	~	S71352	metalloproteinase
15		٠	1070	~	T31069	tolloid-BMP-1 like
16	140.5	7.6	3871	~	T22812	ij
17	139		. 1594	7	T30549	hensin - rabbit
18	137.5	7.4	705	Н	CIHURB	complement subcomp
19	135.5		1464	7	S58984	development protei
20	133.5	٠	402	7	JH0403	procollagen I C-pr
21	128		277	7	A41735	hyaluronate-bindin
22	127		419	7	869207	vascular endotheli
23	125.5	6.8	245	Н	TVCTSS	platelet-derived g
24	125.5		767	7	T30018	hypothetical prote
25	123	6.7	275	7	JC6506	tumor necrosis fac
9₹	119.5	٠,	2083	7	T42721	CRP-ductin-alpha p
27	117.5	6.4	276	7	A47290	TSG-6 homolog PS4
28	117.5	6.4	1290	7	A57190	ebnerin precursor
29	114.5	6.2	200	7	151551	platelet-derived g

platelet-derived g platelet-derived g complement subcomp platelet-derived g pDGF-related trans	complement subcomp 16k vascular endot hypothetical prote UVS.2 protein – Af	plateler-derived g plateler-derived g platelet-derived g platelet-derived g	platelet-derived g vascular endotheli platelet-derived g
S08220 I51550 S05008 PFHUG2 TVWXS	JC6554 D49530 T33161 I51569	S25097 B28964 PFHUG1 JN0248	JS0735 A41551 PFMSGB
881111	0000	7777	177
215 226 241 226	694 148 321 319	225 196 211 166	198 232 241
66.22	လက္လက္ တက္ထဲက်		20.00 20.00
114.5 114.5 113 112.5 111.5	109 108.5 107 104	103.5 103 103 102.5	102.5 102.5 102.5
30 33 34 34	33 34 34 34	39 4 4 4 4 2 2 4 2 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 5 4 5

# ALIGNMENTS

RESULT 1 JC2218
procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN) N;Alternate names: bone morphogenic protein l
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999 C;Accession: JC2218
R; Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Series 134, 257 201, 1353 Affile: Cloning and expression of CDNA encoding Xenopus laevis bone morphogenetic pr
A; Reference number: JC2218; MUID:94085787
A; Accession: JC2218
A; Molecule type: mRNA
A; Residues: 1-707 <mae></mae>
A; Cross-references: GB:L12249; NID:g406540; PIDN:AAA16313.1; PID:g406541
C; Comment: This protein induces ectopic cartilage formation in vivo.
C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology
C; Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F;93-284/Domain: astacin homology <ast></ast>
F;285-397/Region: complement 1r/1s-like repeat
F;285-394/Domain: Clr/Cls repeat homology <c1r1></c1r1>
F;398-510/Region: complement 1r/1s-like repeat
F;398-507/Domain: Clr/Cls repeat homology <c1r2></c1r2>
F;514-550/Domain: EGF homology <egf></egf>
F;554-666/Region: complement 1r/1s-like repeat
F;554-663/Domain: Clr/Cls repeat homology <clr3></clr3>
F;62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F;177/Active site: Glu #status predicted
F;528/Modified site: erythro-beta-hydroxyasparaqine (Asn) #status predicted

Gaps .. 6 Length 707; 33; Indels Query Match 10.3%; Score 191; DB 2; Best Local Similarity 45.2%; Pred. No. 5.6e-08; Matches 47; Conservative 16; Mismatches 33;

5;

55 NGSIHSPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113 g δλ

114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156 δ

Db

# RESULT

procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human N;Alternate names: bone morphogenic protein splice form BMP-1/His C;Species: Homo Saplens (man) C;Dete: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999 C;Accession: A37278; A58788 A58788

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F;130-321/Domain: astacin homology <Asr-
F;322-431/Domain: Clr/Cls repeat homology <CIRI>
F;325-431/Domain: Clr/Cls repeat homology <CIRI>
F;551-587/Domain: EGF homology <EGF>
F;551-700/Domain: Clr/Cls repeat homology <CIR3>
F;91-714,332,335,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644
F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F;214/Active site: Glu #status predicted
                                                                                              A; Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen t
                                                                                                                                                                A;Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homol A;Reference number: JH0466; MUID:91337458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-927 < 778.
A; Cross-references: CAB:D10467; GB:D01077; NID:9222962; PIDN:BAA01260.1; PID:9222963
A; Experimental source: tadpole, brain
A; Note: this protein has motifs homologous to complement components CIr and CIs and t
A; Occomment: This protein is a neuronal cell surface molecule involved in the neuronal
C; Comment: This protein is a neuronal cell surface molecule involved in the neuronal
C; Superfamily: Xenopus A5 antigen; CIr/CIs repeat homology; discoidin I amino-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JQ0948
A5 antigen precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Nenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JH0466; JQ0948
R;Takagi, S; Hirata, T; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| :||| | ||:||:|| || 655 LTADSKLHGKFCGS-EKPEVITSOYNNMRVEFKSDNTV-SKKGFKAHF-----FSEKR 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGSIHSPKFPHTYPRNMVLVWRLVANDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 599 NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 VIISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;861-883/Domain: transmembrane #status predicted <TMM>F;150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Xenopus A5 antigen; LII/LIS Jepent North C; Keywords: duplication; glycoprotein; transmembrane protein E; 1-21/Domain: signal sequence #status predicted <SIG> F; 22-927/Product: A5 antigen #status predicted <A5A> F; 22-927/Product: A5 antigen #status predicted <A5A> F; 27-138/Domain: CIr/Cis repeat homology <CIRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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F;274-424/Domain: discoidin I amino-terminal homology
F;430-584/Domain: discoidin I amino-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%; Score 183.5; DB 1;
30.7%; Pred. No. 3.4e-07;
Live 34; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 183.5; DB
Pred. No. 2.5e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
           A;Cross-references: GDB:125203; OMIM:112264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646-812/Domain: MAM homology <MAM>
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38.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 38.9%
Matches 49; Conservative
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                                                   position: 8p21-8p21
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Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALOPP 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
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R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew Science 242, 1528-1534, 1988
A;Title: Novel requlators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730
A;Accession: A37278; MUID:89072730
A;Molecule type: mRNA
A;Residues: 1-702, EKRPALQPPRGRPHQLKFRVQKRNFTPQ' <WOZ>
A;Cross-references: GB:M22488; NID:9179499; PIDN:AAA51833.1; PID:9179500
B;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encod A;Reference number: A58788; MUID:95096114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;91.142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted F:91.142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted F:163-319,185,205,322-348,375,397,435-461,488-510,551-565,559-572,574-587,591-617,644-66 F:213,217,223,272/Binding site: zinc (His, His, His, His, Tyr) #status predicted F;214/Active site: Glu #status predicted F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen tyn C. Superfamily: procollagen C-endopeptidase; astacin homology; CIr/CIs repeat homology; F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F:33-823/Product: astacin homology <AST>
F:32-431/Domain: CIr/CIs repeat homology <CIRI>
F:435-544/Domain: CIr/CIs repeat homology <CIRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Novel regulators of bone formation: molecular clones and activities A; Reference number: A37278; MUID:89072730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
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A;Cross-references: GB:L35278; NID:g619423; PIDN:AAC41703.1; PID:g619424
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.3%; Score 190; DB 1; 36.0%; Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;551-587/Domain: EGF homology <EGF>
F;591-700/Domain: Clr/Cls repeat homology <ClR3>
F;738-752/Region: histidine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLSGLELLLCPHALVDTVPA--PPSALHGD 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 -----SIIMPQVTETTSPSVLPPSSLSLD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:125203; OMIM:112264
A;Map position: 8p21-8p21
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: BMP1; BMP-1
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A; Residues: 1-730 <WOZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A58788
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A37278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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9

Gaps

15;

Length 730; Indels predicted

9

25; 927;

A; Gene: GDB: BMP1

713

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Length Indels

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procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mous
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Blood 91, 3593-3600, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor, cubilin: Molecular characte
                                                             C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: 149540
B; Noboru, S:; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is A;Reference number: 149540; MUID:94229342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: hydrolase; metalloproteinase; zinc F;135-136/pomain: astacin homology <AST> F;556-592/Domain: astacin homology <AST> F;556-592/Domain: EGF homology <EGI> F;556-705/Domain: CIr/Cls repeat homology <CIR> F;712-747/Domain: EGF homology <EG2. F;218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted F;219/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2173 GHFCGSHASSTLFTSDNQMFVQFISDHSNEGQGFKIKYEAKSLACGGNVYIHDADSAGYV 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Map position: 10p12
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Superfamily: unassigned EGF-related spredicted <SIG>
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F; 436-467/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intrinsic factor-B12 receptor Cubilin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.8%; Score 181; DB 2;
42.6%; Pred. No. 5.9e-07;
tive 16; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%; Score 174.5; DB 2
31.9%; Pred. No. 1.1e-05;
tive 26; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <KO2>
                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: 216677; MUID: 98241400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-991 <RES>
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Best Local 3
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BY ANGOLIAGEN C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human cipecies: Homeo sapiens (mai)

C. Date: 2.2 Mar. 1928 | Sagguence_revision 09-Apr.1998 | *text_change 16-Jul.1999 |
C. Accession: A37218 | BS98 | Sagguence_revision 09-Apr.1998 | *text_change 16-Jul.1999 |
C. Accession: A37218 | BS98 | Sagguence_revision 09-Apr.1998 | *text_change 16-Jul.1999 |
C. Accession: A37218 | BS98 | Sagguence_revision 09-Apr.1998 | *text_change 16-Jul.1999 |
C. Accession: A37218 | BS98 | MUD: 8907230 |
A. Roberter of the company of the c
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                                                                        EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                            NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEF- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              599 NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
                                                                                                                                                                                                                                                  Gaps
IKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHYQRIMINFNPHFDLEDRE----CKYDYV
                                                                                                                                                                                                              --- PSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| : |::||| ||: |::|: || || || 655 LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700
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; Pred. No. 5.9e-07;
16; Mismatches 38;
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llarity 42.6%;
Conservative 1
                                                                                                                                                                                                          166 QVTE--TTSPSVLP-----
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nes 46; Conserv
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Best Local S
Matches 46
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-SPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSD 116

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A Gene: GDB:PCOLCE
A;Cross-references: GDB:305468; OMIM:600270
A;Cross-references: GDB:305468; OMIM:600270
A;Map position: 7q21.3-7q22
C;Superfamily: CIr/CIs repeat homology
C;Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F;1-25-70main: signal sequence #status predicted <ART>
F;37-146/Domain: CIr/CIs repeat homology <CIRI>F;37-146/Domain: CIr/CIs repeat homology <CIRI>F;26/Modified site: pyrrolidone carboxylic acid (GIn) (in mature form) #status predicted F;29,431/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dorsal-ventral patterning protein tolloid (BC 3.4.24.-) - fruit fly (Drosophila melan dorsal-ventral patterning protein tolloid (BC 3.4.24.-) - fruit fly (Drosophila melan dorsal-vents: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A;Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bo A;Reference number: A39288
A;Accession: A39288
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein tolloid; astacin homology; Clr/Cls r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
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                                                                                                                                                                          NID:g642907; PIDN:AAA61949.1; PID:g642908
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A;Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-
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F:221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status
F:222/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.3%; Score 153; DB 1;
Best Local Similarity 33.3%; Pred. No. 0.00014;
Matches 47; Conservative 28; Mismatches 54,
           A; Status: not compared with conceptual translation
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                                                                                                                                                                          A; Cross-references: GB:L33799;
                                                                                                                           <TAK>
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C; Decies: Rattus norvegicus (Norway rat)
C; Decies: Rattus norvegicus (Norway rat)
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: 108618
R; Moestrup, S. K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
A; Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies A; Reference number: 216459; MUID: 98148073
A; Reference number: 216459; MUID: 98148073
A; Rocession: 108618
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rocession: 1-3623 AMDE>
A; Residues: 1-3623 AMDE>
A; Cross-references: EMBL: AF022247; NID: 93834379; PIDN: AAC71661.1; PID: 93834380
C; Genetics:
A; Gene: CUBILIN
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Reywords: e99 yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane F; 1-20/Domain: signal sequence #status predicted <ART>
F; 1-3623/product: intrinsic factor-B12 receptor CUBILIN #status predicted <ART>
F; 436-467/Domain: EGF homology <EGF>>
F; 436-467/Domain: EGF homology <EGF>>
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975 SS-FYLEFHYN--CTNDYLEIYDTAAQTFLGRYCGK-SIPPSLTSNSNSIKLIFVSDSAL 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 DERFGLEDPEDDICKYDFVEVEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYF 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 -----SCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3623;
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                                                                                                                                                                                                                                           2290 APILSKFCGT-SLPSSQWSSGEVMYLRFRSDN-SPTHVGFKAKYSI 2333
                                                                                                                                                                    117 GSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSI 162
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C; Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serin F;1-15/Domain: signal sequence #status predicted <SIG> F;1-44,445-686/Product: Rarreactive factor 2 #status predicted <MAT> F;19-134/Domain: Clr/Cls repeat homology <CIRI> F;142-180/Domain: GGF homology <EGF> F;142-180/Domain: GGF homology <EGF> F;144-293/Domain: Clr/Cls repeat homology <FRI> F;300-361/Domain: complement factor H repeat homology <FRI> F;366-430/Domain: complement factor H repeat homology <FRI> F;45-679/Domain: trypsin homology <TRY> F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-5 F;158/Modified site: erythro-beta-hydroxyasparagine (Assn) #status predicted F;484-445/Cleavage site: Arg-Ile (autolytic) #status predicted F;483,532,633/Active site: His, Asp, Ser #status predicted
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C;Accession: 154763; JN0883
C;Sato, T:, Endo, Y:, Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A;Title: Molecular characterization of a novel serine protease involved in activation
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C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto C; Seywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hy F;1-17/Domain: signal sequence #status predicted <SIG>F;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>F;19-135/Domain: Clr/Cls repeat homology <CIRI>
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F;73:91,443-157,153-166,166-181.185-212,242-266,301-349,322-352,367-414,397-432,436-5
F;55/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
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Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the C1s family of complement proteins found in a bactericida
A;Reference number: JN0883; MUID:94059062
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A;Residues: 1-234, 'E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699 <TAK>
A;Cross-references: DDBJ:DJ7525; NID:9439712; PIDN:BAA04477.1; PID:9439713
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ra-reactive factor (EC 3.4.21.-) 1 precursor - human N;Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFP 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 TDREEHGPFCGK-TLPHRIETKSNTVTITFVTDE-SGDHTGWKIHYT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 SDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;301-362/Domain: complement factor H répeat homology <FH1>F;367-432/Domain: complement factor H repeat homology <FH2>F;449-691/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;490,552,646/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GDB:361104; GDB:330954; OMIM:600521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 145.5; DB 1 Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: MASP1; GDB: CRARF; CRARF1; PRSS5; MASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:143-181/Domain: EGF homology <EGF>
F:185-294/Domain: Clr/Cls repeat homology <C1R2>
F:301-362/Domain: complement factor H repeat homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: I54763; MUID:94289349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vec.,
Best Local Simiları.,
".+rhes 33; Conservative
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A; Residues: 1-699 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I54763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JN0883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
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A5921
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo sapiens (man)
R;Thiel: A second serine protease associated with mannan-binding lectin that activates A;Tefle: A second serine protease associated with mannan-binding lectin that activates A;Tefle: A second serine protease associated with mannan-binding lectin that activates A;Tefle: A status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Status: nucleic acid sequence intoluding the amino end of the mature protein, were dete
C;Genetics:
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
C;Genetics:
A;Gene: GDB:MASP2
A;Cross-references: GDB:6071500
A;Map: position: Lp36.2-lp36.3
C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement factor H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Species: Voct.1999 #sequence_revision 22-oct.1999 #text_change 22-oct.1999
C.Accession: T30337
R.Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
Submitted to the EMBL Data Library, March 1998
A.Specription: CDNA cloning of ovochymase, a chymotrypsin-like protease released from Xe
A.Specrance number: Z20829
A.Accession: T30337
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule EMBL: U81290; NID:92981640; PID:92981641; PIDN:AAC24717.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 DIPTISMLHPRAIALDVCGMAPMIPKWWLPRIVGGEEASPNSWPWQVQIFFLRIFHCEGA 612
                                                                                                                                 432 VSGEVITTQTSRMLLNYVNRNAAKGYRGFK-ARFEVVCGGDLKLTKDQSIDSPNYPMDYM 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-EEP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSDGSVLGRWCGS
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llarity 28.7%; Pred. No. 0.00066;
Conservative 34; Mismatches 73;
                                                                                                                                                                                                                                                                                       GTVPGKQTSKGNHIRIRFVSD 147
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Best Local Similarity
Matches 54; Conserv
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613 IISPQWIL 620
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Job time: 73 sec
                                                                                                                                                                                                                                                                    552 ---IDMKMCG 558
                                                                                                                                                                                                        272 PGCLLVKRCG 281
   459 TTTISTTPV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
$71352
metalloproteinase (EC 3.4.24.-) 10 precursor, blastula - sea urchin (Paracentrotus livid
N;Alternate names: gene tolloid protein homolog
C;Species: Paracentrotus lividus (common urchin)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C;Accession: $71352; A44880; $22060
R;Lhomond, G.; Ghiglione, C.; Lepage, T.; Gache, C.
Eur. J. Biochem. 238, 744-751, 1996
A;Title: Structure of the gene encoding the sea urchin blastula protease 10 (BP10), a me
A;Reference number: $71352; MUID:95300240
A;Reciule type: DNA
A;Residues: 1-597 C-LHO>
A;Cross-references: EMBL:X65721; NID:e956534; PID:e46942
A;Note: the authors translated the codon GCT for residue 11 as Val, AAC for residue 571
B;Lepage, T.; Ghiglione, C.; Gache, C.
Development 114, 14-163, 1992
A;Title: Spatial and temporal expression pattern during sea urchin embryogenesis of a ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A44880; MUID:92249197
A; Reference number: A44880; MUID:92249197
A; Reference number: A44880; MUID:92249197
A; Accession: A44880
A; Status: preliminary
A; Modecule type: mRNA
A; Residues: 1-7, 'S', 9-10, 'V', 12-28, 'H', 30-72, 'D', 74-77, 'SK', 80-81, 'I', 83-232, 'R', 234-239
A; Residues: 1-7, 'S', 9-10, 'V', 12-28, 'H', 30-72, 'D', 74-77, 'SK', 80-81, 'I', 83-232, 'R', 234-239
A; Residues: 1-7, 'S', 9-10, 'V', 12-28, 'H', 30-72, 'D', 74-77, 'SK', 80-81, 'I', 83-232, 'R', 234-239
A; Residues: EMBL: X56224; NID:910929
A; Cross-references: EMBL: X56224; NID:910929
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIP: 99979)
C; Genetics:
A; Correct and a counce:
A; Correct and a coun
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                                                                                                                                                                                                    56 GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEPPS 115
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                                                                                                                                                                                                                                                  29 GQIQSPGYPDSYPSDSEVTWN-ITVPDGFRIKLYF-MHFNLE--SSYLCEYDYVKVE--T 82
                                                                                                                                                                                                                                                                                                                                                                                    116 DGSVLGRWCGSGTVPGKQT ----SKGNHIRIRFVSDEYFPSE---PGFCIHYSII 163
                                                                                                                                     18;
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                                                                  Length 699;
                                                                                                                                     Indels
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F;484-592/Domain: CIr/CIs repeat homology <CIR2>
F;190,194,200/Binding site: zinc (His) #status predicted
F;191/Active site: Glu #status predicted
                                                                                                                                         40;
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                                                               7.8%; Score 144; DB 1;
ilarity 34.7%; Pred. No. 0.00048;
Conservative 19; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTSPSVLPPSSLSLDLLNNAVTAFSTLEELI----
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ses 58; Conserv
                                                                                                     Best Local Similarity
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Matches 58
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
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N'Alternate names: probable metalloprotease TBL-1
C; Species: Aplysia californica (California sea hare)
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 18-Aug-2000
C; Accession: T31069
R; Liu, O.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; J. Neurosci. 17, 755-764, 1997
A; Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by trea A; Accession: T31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC47485.1
C;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 ---CIHYSI------IMPQVTETTSPSVLPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQL----TFDERFGLEDPEDDICKYDFVEVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LSLDLLNNAVTAFS----TLEELIRYLEPDRWQVD---LDSLYKPTWQLLGKAFLYGKK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 LDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 SKVVNLNLLKEEVKLYSC-----TPRNFSVSIREELKRTDTIFWPGCLL-----VKRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 GNCACCLHNCN-----ECQC-----VPRKVTKK---YHEVLQLRPKTGVKGLHKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794 SSNGGCKHICENTVGSFHCSCREGFILADDEKSCKEGGCHYEV-----TDTKGVIQSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 DHGCEHVCVNTLGSYECTCKIGYELHSDGKKCEKACGGYLDAPSGTISSPSFPDLYPPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
7.7%; Score 141.5; DB 2; Length 1070;
Best Local Similarity 20.1%; Pred. No. 0.0013;
Matches 80; Conservative 49; Mismatches 110; Indels 159;
                                        113 --EPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1070 <LIU>
                                                                                                                                                                                                                                                                                                                                   T31069
tolloid-BMP-1 like protein 1 - California sea hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LTDVALEHHEEC
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4.5	Compugen Ltd.
version	- 2000
GenCore	Copyright (c) 1993

OM protein - protein search, using sw model

September Run on:

5, 2001, 10:54:03; Search time 12.6 Seconds (without alignments) 937.948 Million cell updates/sec

US-09-457-066-43 1848

Perfect score:

1 MLLLGLLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched: 93435 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		& Ouerv			SUMMARIES	
No.	Score	Match	Length	DB	ID	Description
-	191	10.3	707	-	BMP1_XENLA	P98070 xenopus lae
7	183.5	6.6	928	Н	NRP1_XENLA	
æ	181		986	Н	BMP1_HUMAN	_
4	181	٠	991	Н	BMP1_MOUSE	_
2	176	9.5	923	٦	NRP1_HUMAN	014786 homo sapien
ø	172	9.3	922	Н	NRP1_RAT	
7	169	9.1	923	1	NRP1_MOUSE	~
00	167		914		NRP1_CHICK	
σ	163.5	8.8	616	-	SPAN_STRPU	strong
10	158	8.5	449	Н	PCO1_HUMAN	
11	155.5	8.4	925	-4	NRP2_RAT	rattu
12	155.5	8.4	931	-	NRP2_HUMAN	O60462 homo sapien
13	155.5	8.4	931	Н	NRP2_MOUSE	O35375 mus musculu
14	153		1057	-	TLD_DROME	P25723 drosophila
15	147.5		704	Н	CRAR_MOUSE	
16	145.5		989	Н	MAS2_HUMAN	
17	144.5	7.8	597	-	BP10_PARLI	-
18	144		669	-	CRAR_HUMAN	P48740 h complemen
19	137.5	7.4	705	Н	C1R_HUMAN	P00736 homo sapien
20	136.5		468	Н	PCO1_RAT	O08628 rattus norv
21	133.5	7.2	468	Н	PCO1_MOUSE	Q61398 mus musculu
22	132		415	Н	VEGC_MOUSE	P97953 mus musculu
23	130		639	Н	BMPH_STRPU	
24	128		277	Н	TSG6_HUMAN	P98066 homo sapien
25	127	6.9	419	Н	VEGC_HUMAN	
56	125.5		245	Н	PDGB_FELCA	
27	117.5		276	Н	TSG6_RABIT	P98065 oryctolagus
28	114.5		226	-	PDGA_XENLA	
58	_		695	Н	CASP_MESAU	
30			241	Н	PDGB_HUMAN	P01127 homo sapien
31			9	Н	VEGF_CAVPO	_
32		٠.	226	Н	TSIS_SMSAV	
33	109	5.9	852		ST14_HUMAN	Q9y5y6 homo sapien

P52585 orf virus ( P49765 homo sapien	P42664 xenopus lae Q05028 rattus norv	Q95229 ovis aries P04085 homo sapien	P20033 mus musculu	P15692 homo sapien	P28576 rattus norv	P52584 orf virus (
VEGH_ORFN7 VEGB_HUMAN	UVS2_XENLA PDGB_RAT	PDGB_SHEEP PDGA_HUMAN	PDGA_MOUSE	VEGF_HUMAN	PDGA_RAT	VEGH_ORFN2
~ <b>~</b>					٠.	Н
148	514 225	241	211	215	204	133
5.9	5.6 5.6	0.0 9.9	5.0 6.0	ຸດ ທີ່ເບີດເ	5.0	5.4
108.5	104 103.5	103.5 $103$	103	102.5	102	100.5
34 35	36	38 39	40	444	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER DIFFERENTIATION OF DEVELOPING ORGANS.
-!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED TADPOLES; LITTLE OR NO EXPRESSION IN WORULA AND LATE GASTRULA.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 3 CUB DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI2A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                       Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.:
"Cloning and expression of cDNA encoding Xenopus laevis bone
morphogenetic protein-1 during early embryonic development.";
Gene 134:257-261(1993).
                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).
                 707 AA
                                                                                                                      laevis (African clawed frog)
                   PRT;
                                                                                                                                                                                                                                         TISSUE=Embryo;
MEDLINE-94085787; Pubmed=8262384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L12249; AAA16313.1; -.
                   STANDARD;
                                                                                                                                                                      Xenopodinae; Xenopus
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=8355;
               BMP1_XENLA
P98070;
                                                                                                                      Xenopus
BMP1_XENLA
```

PROSITE; PS00142; ZINC\_PROTEASE; 1. PROSITE; PS01180; CUB; 3. PROSITE; PS00100; ASX\_HYDROXYL; 1. PROSITE; PS00102; EGF 1; FALSE\_NEG. PROSITE; PS01186; EGF\_2; 1. InterPro; IPR001881; -.
Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 3.
Pfam; PF00008; EGF; 1. PRINTS; PR00480; ASTACIN. InterPro; IPR001506; InterPro; IPR000859;

InterPro; IPR000561; InterPro; IPR000130; InterPro; IPR000152;

MEROPS; M12.005

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5
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E; PS01187; EGF_CA; 1.
factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
                                                                                                                                                                                                                                                                                        EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
"The A5 antigen, a candidate for the neuronal recognition molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               has homologies to complement components and coagulation factors.";
Neuron 7:295-307(1991).
-!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALTIC) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY). PRESUMED TO BE INVOLVED IN ILL. CENTERS.
BETWEEN THE OPTIC NERVE FIBERS AND THE VISIAL CENTERS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
                                                                                                                                                                                                                                                                                                                                              (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Indels
                                                         Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
                                                                                                                                                                       BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 618 LTSDSKLHGKFCGS-ELPAVITSQYNNMRIEFKSDNTV-SKKGF 659
                                                                                                                                                                                                                                                                                                                                                                                                  (BY
(BY
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-1 PRECURSOR (A5 PROTEIN) (A5 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY. SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.3%; Score 191; DB 1;
45.2%; Pred. No. 3.2e-08;
tive 16; Mismatches 33
                                                                                                                                                                                                                                                                                                               CUB.
ZINC (CATALYTIC) (
BY SIMILARITY.
ZINC (CATALYTIC) (
                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog)
Eukaryota, Metazoa, Chordata, Crania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
MEDLINE=91337458; PubMed=1908252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.2%
Marches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
105
295
326
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105
295
326
562
707 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
                                                                                   Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRP1_XENLA
P28824;
                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
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CHAIN
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NRP1_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 VTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : |:| |: ::: || ::: || ECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFA----PKMQEIV--LEFESFELEADS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 QVTE--TTSPSVLP-----PSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDS
                                                                                                                                                                                                                                                                                                 Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 183.5; DB 1; Length 928; 30.7%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF6B323B0A4C789D CRC64;
                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL) CUB 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65;
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Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                              PROSITE: PS00740; MAM_1; 1.
PROSITE: PS01180; CUB: 2.
PROSITE: PS01186; FA58C_1; 2.
PROSITE: PS01286; FA58C_2; 2.
PROSITE: PS50060; MAM_2; 1.
Transmembrane: Glycoprotein; Ne
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Best Local Similarity 30.77
Matches 55; Conservative
                                                                                                                                       InterPro; IPR000421; -.
InterPro; IPR000859; -.
InterPro; IPR000998; -.
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 -: TISSUE SPECIFICITY: UBIQUITOUS.
-: SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-: SIMILARITY: CONTAINS 5 CUB DOMAINS.
-: SIMILARITY: CONTAINS 5 CUB DOMAINS.
-: SIMILARITY: CONTAINS 5 CUB DOMAINS.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
"Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1.";
J. Mol. Med. 76:141-146(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahara K., Lyons G.E., Greenspan D.S.;

"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
are encoded by alternatively spliced transcripts which are
differentially expressed in some tissues.";
J. Biol. Chem. 269:32572-32578(1994).
-!-FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
AND II. INDUCES CARTILAGE AND BONE FORMATION.
-!- CATALYTIC ACTIVITY: CLEAVAGE OF THE C-TERMINAL PROPEPTIDE AT
ALA-|-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-|-ASP IN TYPE
                                                                                                                                                                             Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V., Prockop D.J.; archive that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
-!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C--
ENDOPEPTIDASE ENHANCER PROTEIN.
-!- ALTERNATIVE PRODUCTS: 6 ISOPORMS; BMP1-1, BMP1-2, BMP1-3 (SHOWN
HERE). BMP1-4, BMP1-5 AND BMP1-6; ARE PRODUCED BY ALTERNATIVE
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.19) (BMP-1) (PROCOLLAGEN C-PROTEINASE) (PCP) (MAMMALIAN TOLLOID PROTEIN) (MTLD).
                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                      Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.; "Novel regulators of bone formation: molecular clones and activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 703-986 FROM N.A. (ISOFORM BMP1-3).
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM BMP1-1).
MEDLINE-89072730; Pubmed=3201241;
                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM BMP1-3).
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MEDLINE=95096114; PubMed=7798260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U50330; AAA93462.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              Science 242:1528-1534(1988).
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CAA69975.1;
AAC41710.1;
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PubMed=9500680;
                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                        PubMed=8643539;
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Y08725;
L35279;
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ANGSING (IN ISOFORM BMP1-4).

AACGETTKINGSTISPEMPREYPPRINCIMOLY -> GCY

DLQVGKPLLMDRHCFRLSTHGPEMLGTALRG (IN
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CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
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CUB 3.
EGF-LIKE 2, CALCIUM-BINDING (POFENTIAL).
CUB 4.
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DKDECSKDNGGCQQD -> GGELFGLLGHPPRRP (IN ISOFORM BMP1-6).
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### PF00401; CUB: 5.

### PF00401; CUB: 5.

### PF00401; CUB: 5.

### PF00401; CUB: 5.

### PF0041; CUB: 5.

### PF00411; CUB: 5.

### PF00412; ZUNC_PROTEASE: 1.

### PF0051TE; PS00102; EGF_1; FALSE_NEG.

### PF0051TE; PS01186; EGF_2; 2.

### PF0051TE; PS01186; EGF_2; 2.

### Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Maralloprotease; EGF-1ike domain; Zinc; Calcium; Signal; Jocoprotein; Zymogen; Alternative splicing.

#### SIGNAL 1. PPOTENTIAL.
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D -> N (IN REF. 4).
R -> S (IN REF. 4).
7; F89201913AC3CBEA CRC64;
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(BY
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ZINC (CATALYTIC)
ZINC (CATALYTIC)
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InterPro; IPR000859;
                                                                InterPro; IPR000130;
InterPro; IPR000152;
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MEROPS; M12.005; -.
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                                                         5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMIXME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDOPEPTIDASE ENHANCER PROTEIN.

ENDOPEPTIDASE ENHANCER PROTEIN.

ITSUES PRECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDUUM AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING MEMBRARANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: BELONGS TO REPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                   NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                599 NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΙI
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND II. INDUCES CARTILAGE AND BONE FORMATION.
CATALYTIC ACTIVITY: CLEAVAGE OF THE C-TERMINAL PROPEPTIDE AT
ALA-|-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-|-ASP IN TYPE
                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 41, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-OCT-2000 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Embryo;
MEDLINE=94229342; PubMed=817472;
MEDLINE=94229342; PubMed=817472;
Wagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
which is related to the Drosophila dorsoventral gene tolloid and
encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I,
                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                         ..
8
                            Length 986;
                                                                                                                                             114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                              9.8%; Score 181; DB 1; Length 98
42.6%; Pred. No. 3.2e-07;
tive 16; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY)
                                                                                                                                                                                                                                                991 AA
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L24755; AAA37306.1;
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; M12.005; -
MGD; MGI:88176; Bmp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001881;
                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000561
                                                        46;
                                                                                                                                                                                                                                                BMP1_MOUSE
P98063;
                                                                                                                                                                                                                      SULT 4
                                                                                   55
                                                        Matches
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CUB 2.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604 NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRP1_HUMAN STANDARD; PRT; 923 AA.
014786; 060461;
30-MAY-2000 (Rel. 39, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-1 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRP1 OR NRP OR VEGF165R.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                 PRINTS; PRO0480; ASTACIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00130; CUB; 5.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00020; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 991;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BONE MORPHOGENETIC PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INKED (GLCNAC. . .) (PO 68A1847783A0BB9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
(BY
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BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 181; DB 1; 42.6%; Pred. No. 3.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CATALYTIC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
ZINC (CATALYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUB 3.
EGF-LIKE 2,
                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUB 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUB 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111607 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Conservative
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228
228
353
402
466
515
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622
671
723
747
96
PF00431; CUB; 5.
PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Zymogen
SIGNAL 1 2
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Best Local Similarity
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email to license@isb-sib.ch).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND SOLUBLE/SNRP1; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND
SOLUBLE/SNRP1 ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-
BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT
TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PREDOMINANTLY IN THE
NERVOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN HEART
AND PLACENTA, MODERATELY IN LUNG, LIVER, SKELFTAL MUSCLE, KIDNEY
AND PANCREAS; AND LOW IN ADULT BRAIN. THE SOLUBLE/SNRP1 ISOFORM IS
FOUND IN LIVER HEPATOCYTES, KIDNEY DISTAL AND PROXIMAL TUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR
AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20309748; pubMed=10748121;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";
J. Blol. Cham. 275:18040-18045(2000).
J. Blol. Cham. 275:18040-18045(2000).
FONUTION: THE MEMBRANE-BOUND ISSFORM IS A RECEPTOR INVOLVED IN THE PEVELOPMENT OF CERTAIN NEURONAL CIRCUITS AND IN ORGANGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPUISANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soker S., Klagsbrun M.; "Identification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE SOLUBLE/SNRP1 ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS BY SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gagnon M.L., Bielenberg D.R., Gechtman Z., Miao H.-Q., Takashima S.,
                                                                                                                                                                                                                                                                                                                                                                 Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
                                                                                                                                             He Z., Tessier-Lavigne M.; "Neuropilin is a receptor for the axonal chemorepellent semaphorin
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM), AND SEQUENCE OF 22-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM IS SECRETED..
ALTERNATIVE PRODUCTS: 2 ISOFORMS; MEMBRANE-BOUND (SHOWN HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SOLUBLE/SNRP1 ISOFORM), AND SEQUENCE OF 22-31
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY. SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS. SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000)
                                                                                     SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM) MEDLINE-97433084; Pubmed-9288753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20183929; PubMed=10688880;
                                                                                                                                                                                                                                                                                                                                            MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Prostatic adenocarcinoma
                                                                                                                                                                                                                            Cell 90:739-751(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANGIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity."
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50 VIISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 EVFDGENENGHFRGKFCGK-IAPPPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
EFP -> GIK (IN SOLUBLE/SNRP1 ISOFORM).
MISSING (IN SOLUBLE/SNRP1 ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 QVTE--TTSPSVLP-----PSSLSLDLLNNAVTAFSTLEELIRY----LEPD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 ECSONYTTPSGVIKSPGFPEKYPNSLECTYI---VFAPKMSEIILEFESFDLEPD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                            Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%; Score 176; DB 1; Length 923; 32.6%; Pred. No. 7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D -> H (IN REF. 2).
E -> D (IN REF. 2).
I; ADEADC4A849E5D57 CRC64;
                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> E (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              922 AA
                                                                                                                                                                                                                                                                                                                                                                                                    F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 7.86
24; Mismatches
                                                                                                                                                                                                                                                                                                           NEUROPILIN-1
                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBABLE
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CUB 2.
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EMBL; AF018056; AAC51759.1; -.
EMBL; AF016050; AAC12921.1; -.
                                                                                                                                                               PRINTS; PR00020; MAMDOMAIN.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103120 MW:
                                                                                                               Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C;
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein;
                                       EMBL; AF145712; AAF44344.1;
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                                                                                                      InterPro; IPR000998; -.
                                                                      InterPro; IPR000421; -. InterPro; IPR000859; -.
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54
104
173
228
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300
522
                                                                                                                                                                                                                                                                           Alternative splicing
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749
855
923 AA;
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57; Conserv
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922 AA; 103082 MW; CC6F82AD098B0F2E CRC64;

us-09-457-066-43.Sep5.rsp

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PROSITE; PS01180; CUB; 2.
  SEQUENCE
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NEUROPILIN-1 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
                                                                                     Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                  Neurone; Signal; Repeat; Receptor.
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N-LINKED (GLCNAC.
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TYPE C 2.
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F5/8
                                                           SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-97433085; PubMed-9288754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                CUB
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Pfam: PF00429; MAM; 1.
Pfam: PF00754; F5_F8_type_C; 2.
PRINTS; PR00120; MANDOMAIN.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                              EMBL; AF016296; AAC53337.1; -.
                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01285; FA58C_1; 2. PROSITE; PS01286; FA58C_2; 2. PROSITE; PS00740; MAM 1; 1. PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
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8880
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424
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841
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                                            NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                  fransmembrane;
        RECEPTOR).
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TRANSMEM
DOMAIN
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CARAINEBALB/C; TISSUB-Embryonic brain;

MEDLINE-96353149; PubMed-8748368;

MEDLINE-96353149; PubMed-8748368;

A Kawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Tobelopmentally regulated expression of a cell surface protein,

Tobelopmentally regulated expression with the results in membrane profession of the surface of the surface protein of the regulated expression with the results in the surface of the regulated expression of the regulated expression exp
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                                                                                                                                                                                                                                                                                                                                                                                  62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
                                                                                                Gaps
                                                                                                                                                                                           2 LLLGLLLLTSALAGORTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
                                                                                                                                                                                                                                                                                       7 LLCATLALALALAG-----TIKIENPGYLTSP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                       43 GYPHSYHPSEKCEWLIQAPEPYQRIMINFNPHFDLEDRD---CKYDYVEVIDGENEGGRL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTET-TSPS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                34;
Length 922;
                                                                                           67; Indels
Score 172; DB 1;
Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                                           21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence |
01-OCT-2000 (Rel. 40, Last annotation NEUROPILIN-1 PRECURSOR (A5 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
    9.3%;
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                                                                                                56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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InterPro; IPR000859; -.
InterPro; IPR000998; -.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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P97333;
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Dev. Biol. 170:207-222(1995).
-!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CARDIOVASCULAR SYSTEM, IN ANNIOGENESIS, IN THE FORMATION OF
CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-WHITE LECHORN: TISSUE-Embryonic brain;
MEDLINE-95324761; PubMed-7601310;
Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,
Fujisawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LLCATLALALALAG-----TIKIENPGYLTSP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 GYPHSYHPSEKCEWLIQAPEPYQRIIINFNPHFDLEDRD---CKYDYVEVIDGENEGGRL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTET-TSPS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                              Neurone; Signal; Repeat; Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Indels
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                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC...
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Pred. No. 2.9e-06;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-1 PRECURSOR (A5 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC
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                                                                                                                                                                                                                                                                                         F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                                           NEUROPILIN-1
                                                                                                                                                                                           POTENTIAL.
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Best Local Similarity 31.5%;
Matches 56; Conservative 21
                                                                                              Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
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424
424
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261
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522
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923 AA;
                   PS01286; F
PS00740; N
PS50060; N
PS01285;
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P79795;
                                                                                                                                              CHAIN
DOMAIN
TRANSMEM
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DISULFID
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                      PROSITE;
                                                                                                                       SIGNAL
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AC NRP1_CHICK
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DT O1-NOY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 167; DB 1; Length 914;
28.8%; Pred. No. 4.3e-06;
.ive 31; Mismatches 65; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q.
                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: DEVELOPING NERYOUS SYSTEM; OPTIC TECTUM
TISSUE SPECIFICITY: DEVELOPING NERYOUS SYSTEM; OPTIC TECTUM
CLAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES OF
DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONBEURONAL CELLS, E.G.
BLOOD VESSELS IN THE ENTIRE EMBRYO.
SIMILARITY: BELONGS TO THE NURROPPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 FS/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 ECSRNFTSSSGMIKSPGFPEKYPNSLECTYIIFAPKMSEIILEFESFE----LEPD 195
SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00020; MAMDOMAIN.
PROSTIE: PS01180; CUB; 2.
PROSTIE: PS01286; FA58C_2; 2.
PROSITE; PS01240; MAM_1; 1.
PROSTIE: PS050060; MAM_2; 1.
Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 QVTE--TTSPSVLP-----PSSLSLDL-----LNNAVTAFSTLEELIRYLEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
DD2EE6D6F0CBB68C CRC64;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
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TYPE C 2.
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BY
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InterPro; IPR000959; -.
InterPro; IPR000998; -.
Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
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Best Local Similarity 28.8%
Matches 51; Conservative
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914 AA;
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RESULT 9 SPAN\_STRPU

Similarity

Best Local

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C., "Early mRNAs, spatially restricted along the animal-vegetal axis of sea urchin embryos, include one encoding a protein related to tolloid
                                                                                            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                        Development 114:769-786(1992).
-!- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS
OF THE BLASTULA.
                                                                                                                                                                                                                                                            -! - DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
( SIMILARITY.
( SIMILARITY.
397CD923FFB9EB98 CRC64;
                                                                                 Strongylocentrotus purpuratus (Purple sea urchin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARG/LYS-RICH (BASIC)
                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SPAN PROTEIN PRECURSOR (EC 3.4.24.-).
 616 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METALLOPROTEASE
                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPAN PROTEIN.
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                                                                                                                                                                  MEDLINE=92315921; PubMed=1618141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000130; -. InterPro; IPR000561; -.
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93
295
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                                                                                                                      Strongylocentrotus.
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616 AA;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         AND HATCHING)
                                                                                                                               NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; M12.013;
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94
89
94
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340
451
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SPAN_STRPU
P98068;
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11;
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MEDLINE=95014462; PubMed=7523404;
Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,
Janl-Sait S., Shows T.B., Greenspan D.S.;
Type I procollagen COOH-terminal proteinase enhancer protein:
identification, primary structure, and chromosomal localization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Heart;
Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,
Morisaki N., Saito Y.;
"Smooth muscle cell derived procollagen C-protease enhancer protein.";
Cell Struct. Funct. 21:662-662(1996).
                                                                                                                                                                                                                    95 GLEDPEDDICKYDFVEVEPEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPS-- 152
                                                                                                                                                                                                                                                        439
                                                                                                                                                                                                                                                                                                                                                                                                                           PCO1_HUMAN STANDARD; PRT; 449 AA.
Q15113, 014550;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR (PCPE) (TYPE I PROCOLLAGEN COH-TERMINAL PROTEINASE ENHANCER) (TYPE I PROCOLLAGEN COH-TERMINAL PROTEINASE ENHANCER)
                                                                                               269 INSRL-GQRTALSAADIELANRIYECDDVEDCSNADECLNGGYHDADCDCVCPSSYSGDL 327
                                  Gaps
                                                                    9 LTSALAGORTG-TRAESNLSSKLQLSSDKE-----QNGVQDPRHERVV--TISGN- 55
                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsui L.-C., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Placenta;
MEDLINE-99134301; PubMed-9933570;
MEDLINE-99134301; PubMed-9933570;
Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
Structural organization and expression patterns of the human and mouse genes for the type I procollagen COOH-terminal proteinase enhancer protein.";
                                                                                                                                                                    328 CQDGGPTVRPADCSYRFTEMTGEITSPNYPSNYEDNTACVYEIEG-PYGSTIELTF---L
                                                                                                                                                                                                                                         384 DMEIETETLCRYDAVEVRKDDINSIGEKECGN-TLPPVQISSSNQMAVSFTSD---PSIT
                                                                                                                                             -----GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gloeckner G., Scherer S., Schattevoy R., Boright A., Weber J., Tsui L.-C., Rosenthal A.;
             5.1e-06;
thes 85; Indels
                                                                                                                                                                                                                                                                                              195
                                                                                                                                                                                                                                                                                              153 EPGFCIHYSIIMPQVT--ETTSPSVLPPSSLSLDLLNNAVTAFST
                                                                                                                                                                                                                                                                                                                                 440 RRGFKATYVIIIQTTTVFSTTTLQTTPPSTTTLQTTNPSTTTLQT
             Pred. No. 5.16
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished observations (FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99018118; PubMed=9799793;
28.08; Pic. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reveals 17 genes.";
Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO 56; 154 AND 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEINASE ENHANCER PROTEIN)
                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                     Proceduras enhancer releases a metalloproteinase inhibitor.";

proteinase enhancer releases a metalloproteinase inhibitor.";
J. Biol. Chem. 275:1384-1390(2000).
-!- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE I
PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
-!- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN METALLOPROTEINASE INHIBITORY ACTIVITY.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- FUNCTION: C-BERMINALLY PROCESSED AT MULTIPLE POSITIONS.
-!- SIMILARITY: CONTAINS 1 UTR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20092917; PubMed-10625689;
Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLEAVAGE.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

3D88430158648796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                              PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN.
                   PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 158; DB 1;
34.5%; Pred. No. 9.7e-06;
iive 21; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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CLEAVAGE.
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CUB 2.
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EMBL; AB0008549; BAA23281.1; -.
EMBL; AP053356; AAA78800.1; -.
EMBL; AF083655; AAD16041.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 -- PQVTETTSPSV-LPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000859; -.
InterPro; IPR00134; -.
Fram: PF00431; CUB; 2.
Pfam: PF01759; NTR: 1.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47972
Genomics 55:229-234(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 34.5
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            288
289
294
300
304
431
                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal.
SIGNAL 1 25
                                                                                                                                                                                                                                                                                                                                                                                                                    288
293
299
303
431
449 AA;
                                                                                                                                                                                                                                                                                                                                                                                         159
329
287
                                                                                                                                                                                                                                                                                     MIM; 600270; -
                                               Banda M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
NRP2_RAT
ID NRP2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                             SITE
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SITE
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925 AA

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE LINING IN THE RIBS.
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-2 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F5/8 TYPE C 1.
F5/8 TYPE C 2.
MAM.

BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
MM; 3BF62903F64485IC CRC64;
                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rat
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurone; Signal; Repeat; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINING IN THE KIBS.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                        Ginty D.D.;
"Neuropilin is a semaphorin III receptor.";
Cell 90:753-762(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEUROPILIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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CUB 2.
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InterPro; IPR000421; -.
InterPro; IPR000859; -.
InterPro; IPR00098; -.
Pfam; PF00431; CUB; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00754; F5_F8_type_C; 2. PROSITE; PS01180; CUB; 2. PROSITE; PS01285; FA58C_1; 2. PROSITE; PS51286; FA58C_2; 2. PROSITE; PS50060; MAM_2; 1.
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                                                                                                                                                                         Rattus norvegicus (Rat)
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267
267
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105
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230
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1152
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833
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925 AA;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                   RECEPTOR 2)
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149
208
277
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CHAIN
DOMAIN
TRANSMEM
DOMAIN
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Matches
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NRP2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
MEDLINE=97470888; PubMed=9331348;
Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
"Neuropilin-2, a novel member of the neuropilin family, is a high
affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                 QDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPED 101
                                                                                                                                                  102 DICKYDFVEVEPPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIH 159
                                                                                                                                                                      --CKYDFIEIRDGDSESADLLGKHCGN-IAPPTIISSGSVLYIKFTSD-YARQCAGFSLR 138
                                                   Gaps
                                                                                                      24 QDPPCGGRLNSKDAGYITSPGYPQDYPSHQNCEWVYAPPEPUQKIVLNFNPHFEIEKHD- 82
                                                                                                                                                                                                                                                                                                                                                        Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRP2 OR VECF165R2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                 7;
               Length 925;
                                                 Indels
                               .9e-05;
                                                                                                                                                                                                                                                                                                                                             931 AA
                                               19; Mismatches
            Score 155.5;
Pred. No. 3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM A22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98188099; PubMed=9529250;
               8.48;
                                                 41; Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuron 19:547-559(1997).
          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                       160 YSI 162
                                                                                                                                                                                                                                                         YEI 141
                                                                                                                                                                                                                                                                                                                       NRP2_HUMAN

ID NRP2_HUMAN

ID NRP2_HUMAN

O 060462; 0148

DT 01-0CT-2000

DT 01-0CT-2000

DE NEUROPILIN-20

OS NEUROPILIN-2)

CO EURATYOLE; M

OC MAMMALIA ED

RR SQUENCE FRC

RR MEDLINE-974

RR Chen H., Che

RR MEDLINE-974

RR Chen H., Che

RR T Neuropilin-

RT Affinity rec

RT TII."; TA

RR SCOUENCE FRC

RR TIII."; TA

RR SCOUENCE FRC

RR III."; TA

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RR III."; TA

RR SCOUENCE FRC

RR III."; TA

RR SCOUENCE FRC

RR GLISSUE-BREAS

RR CHARACTERIZI

RR SCOUENCE FRC

RR GLISSUE-BREAS

RR GLISSUE-BREAS

RR GLISSUE-BREAS

RR GLISSUE-BREAS

RR GLISSUE-BREAS

RR JSOCOM-SPC

RR GLISSUE-BREAS

CC --- SUBCELLIC

CC --- SUBCELLIC

CC --- SUBCELLIC

CC --- SUBCELLIC

CC --- SIMILAR

CC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 SRHQVRGQPDPPCGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRP2_MOUSE STANDARD; PRT; 931 AA.
035375; 035374; 035376; 035377; 035378;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
NEUROPILIAL PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
RECEPPOR 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%; Score 155.5; DB 1; Length 931; 32.1%; Pred. No. 3.9e-05; ive 20; Mismatches 62; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E -> K (IN REF. 1).
MW; 270CBAE69A0A797C CRC64;
      Usage by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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N-LINKED (GLCNAC...) (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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F5/8 TYPE C 2.
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                                                                                                                                                                                                                             Pfam; PF00431; CUB; 2.
Pfam; PF00529; MAM; 1.
Pfam; PF00754; F5_F8_type_C; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUB
                                                                                EMBL; AF022859; AAC51788.1; -. EMBL; AF022860; AAC51789.1; -. EMBL; AF016098; AAC12922.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 32.19
nes 42, Conservative
                                                                                                                                                                 InterPro; IPR000421; -.
InterPro; IPR000859; -.
InterPro; IPR000998; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 SEPGFCIHYSI 162
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us-09-457-066-43.Sep5.rsp

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SEQUENCE FROM N.A.
DISULFID
                                                            CARBOHYD
                                                                               CARBOHYD
                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          NEUTON 19:547-559(1997).

-I FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOFORMS OF VEGF, AND THE PICE-2 ISOFORM OF PGF.

-I SUBUNT: NEUROPILIN-2 PROBABLY FORMS AN HETEROWERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.

-I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I ALTERNATIVE PRODUCTS: 6 ISOFORMS; A22 (SHOWN HERE), A0, A5, A17,

BO AND B5; ARE PRODUCED BY ALTERNATIVE SPLICING.

-I TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME
NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,

INTESTINAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND

IS DEVELOPMENTAL REGULATED.
                                                                                                                                                                                Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.; "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                     Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUROPILIN-2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY. SIMILARITY: CONTAINS 2 CUB DOMAINS. BIMILARITY: CONTAINS 2 E5/8 TYPE C DOMAINS. SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                       SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
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F5/8 TYPE C 2.
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                                                                                                                                                               MEDLINE=97470888; PubMed=9331348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000998; -.
Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01286; F858C_1; 2.
PROSITE; PS01286; F858C_2; 2.
PROSITE; PS00609; MAM_Z; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY
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BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF022857; AAC53380.1; -. EMBL; AF022858; AAC53381.1; -. EMBL; AF022861; AAC53382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1100492; Nrp2.
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8884
8889
931
142
267
267
862
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105
175
230
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                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative splicing
                                                                               WCBI_TaxID=10090;
                                                                                                                                        STRAIN-BALB/C
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DOMAIN
TRANSMEM
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BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

MISSING (IN ISOFORM A17).

MISSING (IN ISOFORM A17).

MISSING (IN ISOFORM A5).

MISSING (IN ISOFORM A5).

SGKEKVDIPETHGGEGYEDEIDDEYEDDWSNSSSSTSGAGDP
SSGKEKSWLTLDFILITIIAMSSLGVLLGATCAGLLLYT
CSYSGLSSRSCTTLEBYNFELYDGLKHKVKINHQKCCSEA.

SGTLPPGTEEPTVDTVPVQDIPAYWYYWAAGGAVLULAS.
                                                                                                                                                                                                                                                                                                                                       VVALVLHYHRRYAAKKTDHSITYKTSHYNGADAVEDY
LTIKLEQERGSHC (IN ISOFORM B0).
VDIPETHGGEVEDELDEDENDSNSSSSTSGADDSSGK
EKNWIYTLDPILLITAMSSLGVLLGATCAGLLLYTCSYG
GLSSRSCTTLENYNFELYDGLKHKVKINHOKCCSEA -> G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLPPGTEPTVDTVPVQPIPAYWYYVMAAGGAVLVLASVVL
ALVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 FGLEDPEDDICKYDFVEVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-2014970; PubMed-1840509;
MEDLINE-2014970; PubMed-1840509;
Shimell M.J., Ferguson E.L., Childs S.R., O'Connor M.B.;
"The Drosophila dorsal-ventral patterning gene tolloid is related to
human bone morphogenetic protein 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 SGHEVRSQODPPCGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLD_DROME STANDARD; PRT; 1057 AA.
P25723; Q9V046;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
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Finelli A.L., Bossie C.A., Xie T., Padgett R.W.;
"Mutational analysis of the Drosophila tolloid gene, a human BMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLEQERGSHC (IN ISOFORM B5)
G -> I (IN AAC53380 AND AAC53381).
7; 76F2443F411D2F63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%; Score 155.5; DB 1; Length 931; 32.8%; Pred. No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development 120:861-870(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 32.89
Matches 43; Conservative
     427
592
152
157
157
629
839
830
830
830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 SEPGFCIHYSI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 QGAGFSLRYEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                931 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                              VARSPLIC
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VARSPLIC
                             DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
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PR00480; ASTACIN.

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RESULT 15
CRAR_MOUSE
     DORN NEW WELL OF STATE OF STAT
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          RAY MEDELINE—20196006; PubMed=10731132;

RAMIN = LEMENTELEY;

RAMIN = LEMENTER = LEME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: REQUIRED FOR NORMAL DORSAL DEVELOPMENT. TLD MAY INTERACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: MUTATIONS IN TLD GENE LEAD TO A PARTIAL TRANSFORMATION OF DORSAL ECTODERM INTO VENTRAL ECTODERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHYSICALLY WITH DPP-C PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: M76976; AAA28491.1; -.
EMBL: U04239; AAC46482.1; -.
EMBL: AEU03749; AAF56329.1; -.
PIR; A39288; A39288.
HSSP; P00742; 1FAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0003719; tld
InterPro; IPR000130; -.
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PF00431; CUB; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000561; - InterPro; IPR000859; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .nterPro; IPR001506; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; M12.010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00008;
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Pfam; |
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7
PROSITE; PRO0142; ZINC_PROFEASE; 1.
PROSITE; PS01042; ZINC_PROFEASE; 1.
PROSITE; PS01080; CUB; 5.
PROSITE; PS010010; ASX_HINDROXYL; 2.
PROSITE; PS01025; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
PROFILE; PS01187; EGF_CA; 2.
PROFILE; PS01187; EGF_CA; 2.
POFFORTIAL: Signal; Repeat; Zymogen.
I 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 RNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSDGSVLGRWCGS 126
                                                                                                                                                                                                                                                                                                                                EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LAGORIGIRAESNLSSKLQLSSDKEQNGVQDPRHERV----VTISGNGSIHSPKFPHTYP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC (CATALITI).

ZINC (CATALITIC) (BY SIMILARITY).

ZINC (CATALITIC) (BY SIMILARITY).

CELL ATTACHMENT SITE (POTENTIAL).

BY SIMILARITY.

BY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                          DORSAL-VENTRAL PATTERNING TOLLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                       (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 153; DB 1; Length 1057; Pred. No. 7.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76F4B5AEB7996FBA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                                                                                                                                                                                                                                METALLOPROTEASE
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ZINC (CATALYTI)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7.3e
28; Mismatches
                                                                                                                                                                                                      POTENTIAL
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547 KLPPNIKT-RSNQMYIRFVSD 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GTVPGKQTSKGNHIRIRFVSD 147
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33.3%;
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1057
                                                                                                                                                                                                                                                                908 90
1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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407
468
522
585
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ACT_SITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 190:681-687(1993).
-!- FUNCTION: COMPONENT OF THE BACTERICIDAL RA-REACTIVE FACTOR RARF WHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED BY CERTAIN ENTEROBACTERIA. IT TRIGGERS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takayama Y., Takada F., Takahashi A., Kawakami M.;
"A 100-kDa protein in the C4-activating component of Ra-reactive factor is a new serine protease having module organization similar to C1r and C1s.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=93176166; PubMed=8439319;
Takahashi A., Takayama Y., Hatsuse H., Kawakami M.;
"Presence of a serine protease in the complement-activating component of the complement-dependent bactericidal factor, RaRF, in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C4 COMPONENT BY CLEAVING THE ALPHA-CHAIN OF C4.
SUBUNIT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT
(CRARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT.
CRARF IS AN HETERODINER OF A HEAVY (P70) AND A LIGH CHAIN (29)
LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: LIVER.
DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO CIR AND CIS.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                       PRECURSOR
                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
COMPLEMENT-ACTIVATING COMPONENT OF RA-REACTIVE FACTOR PRECURSO
(EC 3.4.21.-) (RA-REACTIVE FACTOR SERINE PROTEASE P100) (RARF)
(MANNAN-BINDING LECTIN SERINE PROTEASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 465-704 FROM N.A., AND PARTIAL SEQUENCE
704 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 • Pfam; PF00084; sushi; 2.
• Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94179811; PubMed=8133044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 152:2308-2316(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/C; TISSUE=Liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D16492; BAA03944.1;
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InterPro; IPR000859; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
InterPro; IPR001881; -.
Pfam; PF00431; CUB; 2.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.198; -. MGD; MGI:88492; Maspl. InterPro; IPR000152; InterPro; IPR000436; -
                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS01186; CUB; 2.
PROSITE; PS01186; EGF_2; 1.
Hydrolase; Complement pathway; Serine protease; Protease; Glycoprotein; Sushi; Repeat; Signal; EGF-11ke domain; Hydroxylation.
                                                                                                                                        EGF-LIKE, CALCIUM-BINDING (POTENTIAL)
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SIMILARITY).
SIMILARITY).
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                                                                                 COMPLEMENT-ACTIVATING COMPONENT
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22.5%; Pred. No. 0.00013;
Live 59; Mismatches 128; Indels
                                                                                            RA-REACTIVE FACTOR (P100).
70 KDA CHAIN OF P100 (P70)
29 KDA CHAIN OF P100 (P29)
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Best Local Similarity 22.55
Matches 75; Conservative
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Search completed: September Job time: 122 sec

09qx38 rattus norv

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091674 xenopus lae 097270 homo sapien 095570 homo sapien 096510 homo sapien 026051 paracentrot 096401 cyprinus ca 096900 cyprinus ca 0969vy2 triakis scy
                       057382 xenopus lae
043897 homo sapien
Q9nqs4 homo sapien
070244 rattus norv
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09dgc2 cyprinus ca

009020 rattus norv

09jjs9 rattus norv

001654 halocynthia

091674 xenopus lae
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TISSUE-OVARY:

Taai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

Taai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

Taai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

Town cloud of fallotein from mouse ovary.";

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

REBL; AF117608; AAF22516.1;

RINGEPRO: IPRO00052;

Refan: PF00431; CUB: 1.

REPOSITE: PS01180; CUB: 1.

REPOSITE: PS01180; CUB: 1.

REPOSITE: PS0128 PDGF_2: 1.

REPOSITE: SANO042; CUB: 1.

SARART: SM00042; CUB: 1.

SEQUENCE 345 AA; 38741 MW; 3A58AIF701B84EAZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Verdaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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Last annotation update)
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           Q62381
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Q9QY71;
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01-MAY-2000 (TEMBLEEL 13,
01-MAY-2001 (TEMBLEEL 16,
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                                                                                                                                                                          1 MLLLGLLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                            2001, 10:54:03
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Maximum Match 100%
Listing first 45 summaries
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tsai Y.J., Lee R.K.K., Lin S.P.;
"Fallotein, a novel growth factor like gene identified in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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Biochem. Biophys. Res. Commun. 0:0-0(2000)..
EMBL; AB033830; BAB19969.1; -.
SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;
                                                                                                                                                                                                                                                                                  STRAIN-WISTAR, TISSUE-KIDNEY,
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor
                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                             SPINAL CORD-DERIVED GROWTH FACTOR.
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                                                     PRELIMINARY;
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                                                                                                                                                                                Rattus norvegicus (Rat).
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01-MAR-2001
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01-MAR-2001
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                   LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECOCVPRK
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                                  LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=SWLSS-WEBSTER/NIH;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
"The mouse Pdgfc gene: Dynamic expression in embryonic tissues
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
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Pred. No. 1.5e-156;
0; Mismatches 4;
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PROSITE; PFO1180; CUB; 1.
PROSITE; PF02078; DGFC 2; 1.
SEQUENCE 345 AA; 38886 MW:
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98.8%;
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EMBL, AF286725; AAF91483.1;
InterPro; IPR000072; -.
InterPro; IPR000859; -.
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Best Local Similarity
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01-MAR-2001 (
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SEQUENCE
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                                                                                                                         Hamada T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the POGF/PEGF family.";
EMBL: AF0914134; AAF0004991: -.
EMBL; AB033831; BAB03266.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL, AF244813; AAF80597.1; -.
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                        to the EMBL/GenBank/DDBJ databases.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
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                                                                                   TISSUE-BRAIN;
MEDLINE=20317014; PubMed=10858496;
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InterPro; IPR000072; ...
Pfam; PF00341; PDGF; 1.
Pfam; PF00431; CUB; 1.
PROSITE; PS01180; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00042; CUB; 1.
SEQUENCE 345 AA; 39029 MW; C
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SEQUENCE FROM N.A.
STRAIN=WHITE LEGHORN; TISSUE=SPINAL CORD;
MEDLINE=2031704; PubMed=10858496;
MEDLINE=20317014; PubMed=10858496;
Memda T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
FEBS Lett. 475:97-102(2000).
INTERPROS PRO30007:
InterPro; IPR000859; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LIEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                          61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEVEPSDGTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                                                                                               590889CEA55CC5EA CRC64,
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                                                                                                                                                                                                              ; Score 1664; DB 4;
; Pred. No. 1.6e-142;
28; Mismatches 18;
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Pred. No. 2.2e-132;
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InterPro; IPR000072; -.
InterPro; IPR000859; -.
Pfam; PF00431; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
SMART; SM0042; CUB; 1.
SEQUENCE 345 AA; 39043 MW; 5
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86.78;
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PROSITE; PS50278; PDGF_2; 1.
SMART; SM00042; CUB; 1.
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80.3%;
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Best Local Similarity 86.7%
Matches 299; Conservative
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(TrEMBLrel. 06, (TrEMBLrel. 06,
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                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                               NCBI_TaxID=9606;
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057658;
01-JUN-1998 (
01-JUN-1998 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 PGFCIHYSII---MPQ-----VTET----TSPSVLPPSSLSLDLLNNAVTAFST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP-- 313
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   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                          MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVT1SGNGSIHS
                                      PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                                                          GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                                         LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
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                                                                                                                                                                           181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEQUENCE FROM N.A.
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
Holecular Cloning of SCDGF-B, a Novel Growth Factor Homologous SCDGF/PDGF-C/Fallotein.";
Blochem. Biophys. Res. Commun. 0:0-0(2000).
EMBL; AB052170; BAB18920.1; -.
SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.8%; Score 754; DB 11; Length 370;
46.2%; Pred. No. 4.1e-60;
tive 62; Mismatches 86; Indels 2
   Indels
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Last annotation update)
   31;
  37; Mismatches
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01-MAR-2001 (TrEWBLrel. 16, Last ann
SPINAL-CORD DERIVED GROWTH FACTOR-B.
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Matches 277; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 151; Conserv
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01-MAR-2001
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TISSUE-AORTA;
Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu B., Liu Y.Q., Wang X.Y., Zhang C.L., Zhang J., Wei Y.J.,
Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033832; BAB18903.1; -.
EMBL; AR113216; AA339287.1; -.
EMBL; AR113216; AA339287.1; -.
EMBL; AR113216; AA339287.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036)
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; Pred. No. 6.3e-60;
59; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCDGF/PDGF-C/fallotein.";
Biochem. Biophys. Res. Commun. 0:0-0(2000)
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314 -KTGVKGLHKSLTDVALEHHEECDCVC 339
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                                   338 FKRRGKAKNMALVDIQLDHHERCDCIC
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EMBL; D83476; BAA11922.1;
HSSP; P00736; 1APQ.
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InterPro; IPR000859; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium-binding;
                                                 MEROPS; M12.015;
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"Xtld, a Xenopus homolog of dorso-ventral polarity gene in Drosophila,
modifies tissue phenotypes of the ventral mesoderm.",
submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00042; CUB; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 NGSISSPGWPRDYPPNKHCVWQLVAPTQ-YRISLRFD---FFFFTEGNDVCKYDFVEVRSG 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTS 172
                                                                                                 Eukaryoťa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                       Reynolds S.D., Puzas J.E., O'keefe R.J., Rosier R.N., Reynolds P.R.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. EMBLSI; J. 3331; AAC02259.1; -. HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 192.5; DB 13; Length 691; 38.6%; Pred. No. 6.3e-09; Live 21; Mismatches 46; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691 AA; 77843 MW; 01245982B8DC8F28 CRC64
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01-NOV-1996 (TrEMBLrel.-01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 16, Last annotation update)
XTLD PROYERN.
Xenopus laevis (African clawed frog).
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001506; -.
Interpro; IPR001801; -.
Pfam; PF00431; CUB; 3.
Pfam; PF00431; CUB; 3.
Pfam; PF00400; Astacin; 1.
PRINTS; PR00400; ASTACIN.
PROSITE; PS01100; ASX_HYDROXYL; 1.
PROSITE; PS01180; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 38.6 les 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                         Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000130; -.
InterPro; IPR000152; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000859; -.
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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671 PPQIPPA 677
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                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                        MEROPS; M12.005
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SEQUENCE
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Q91925;
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DDR RRAP DDR RAP D
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nding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat. 977 AA; 110199 MW; 4D7D2E37C64FDFIF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBL_TaxID-8355;
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6
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DAV. Biol. 0:0-0(0).
EMBL; X09660; CAA70853.1; -.
HSSP; P007765; JAPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.3%; Score 191; DB 13; Best Local Similarity 45.2%; Pred. No. 1.4e-08; Matches 47; Conservative 16; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001506; ...
InterPro; IPR001881; ...
Pfam; PF00008; EGF; 1.
Pfam; PF00401; CUB; 3.
PRINTS; PR00480; ASTACIN.
PROSITE; PS01180; CUB; 3.
PROSITE; PS01180; CUB; 3.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
MERCES; MLZ.103; ...
InterPro; IPR000130; ...
InterPro; IPR000152; ...
InterPro; IPR000152; ...
InterPro; IPR000859; ...
InterPro; IPR001891; ...
InterPro; IPR001881; ...
Pfam; PF00008; EGF; 2...
Pfam; PF00408; EGF; 2...
Pfam; PF01400; Astacin; 1...
PROSTIE; PS001010; ASX_HYDROXYL; 2...
PROSTIE; PS01180; CUB; 5...
PROSTIE; PS01180; CUB; 5...
PROSTIE; PS01187; EGF_2; 2...
PROSTIE; PS01187; EGF_2; 2...
PROSTIE; PS01187; EGF_CA; 2...
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PROSITE; PS01187; EGE-
PROSITE; PS00142; ZING
SMART; SM00042; CUB;
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595 LSPDAKLHGRFCGSET-PEVITSQSNNMRVEFKSDNTV-SKRGFRAHF 640
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SEQUENCE FROM N.A.
                                                                                                                                                                                                      TISSUE-PLACENTA;
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                                                       Q9Y6L7
Q9Y6L7;
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                                  RESULT 13
Q9Y6L7
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                                                                                                                                                                                                                                                                                                                                                                               Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Miyajima N., Tanaka A., Kotani H., Nomura O.;
Tradiction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:63-70(1999).
EMBI: AB033149; BAA76776.1; -.
HSSP; P00736; 1APQ.
Calcium-binding; EGF-1ike domain; Glycoprotein; Hydroxylation; Repeat. SEQUENCE 735 AA; 83575 MW; 45b29C813F79DBE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00042; CUB; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
                                                                                         NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
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                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8
                                           10.1%; Score 186; DB 13; Length 735; 45.2%; Pred. No. 2.6e-08; ive 15; Mismatches 34; Indels
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10.0%; Score 185; DB 4; Length 926;
Best Local Similarity 45.4%; Pred. No. 4.4e-08;
Matches 49; Conservative 14; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58FA35CDDE10970B CRC64;
                                                                                                                                  114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156
                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 926 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0480; ASTACIN.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS01180; CUB; 5.
PROSITE; PS01187; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
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                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99246063; PubMed=10231032;
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                                                                                                                                                                                                                                                                     KIAA0932 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01400; Astacin; 1.
                                  Ouery Match
Best Local Similarity 45.2%
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000130; -. InterPro; IPR000152; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; -
InterPro; IPR000859; -
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                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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SEQUENCE
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Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat. SEQUENCE 1015 AA; 113556 MW; 25F5B23065861593 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           Scott I.C., Greenspan D.S.;
"Sequence of the human mammalian tolloid-like 2 (n
chromosomal localisation of the cognate gene TLL2.
Dev. Biol. 0:0-0(1999).
EMBL; RF05916; AD42979.1; -
PRT; 1015 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0480; ASTACIN.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS01180; CUB; 5.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                Created)
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                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2001 (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001881; -. Pfam; PF00008; EGF; 2. Pfam; PF00431; CUB; 5. Pfam; PF01400; Astacin; 1.
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PRELIMINARY;
                                                                   01-NOV-1999 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
TOLLOID-LIKE 2 PROTEIN.
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InterPro; IPR000859; -
InterPro; IPR001506; -
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Best Local Similarity
Matches 49; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00042; CUB;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PROSITE; PROMONO, ASTACIN.
PROSITE; PROMONO, ASTACIN.
PROSITE; PROMONO, ASTACIN.
PROSITE; PROMONO, EGF_2; 2.
PROSITE; PROMONO, EGF_CA; 2.
PROSITE; PROMONO, EGF_CA; 2.
SMART; SMOMONO, EGF_CA; 2.
SMART; SMOMONO, EGF_LIKE domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 1012 AA; 113252 MW; 72EEE268A4D8C5FE CRC64;
Thomas C.L., Scott I.C., Maas S.A., Clark T.G., Greenspan D.S., "Sequence of murine mammalian tolloid-like-2 (mTll-2) and chromosomal localization of the cognate gene Tll2.";

Dev. Biol. 0:0-0(1999).

EMBL: AF073226; AAD42993.1;

HSSP: P00742; 1HCG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
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TISSUE=TESTIS;
Hirahara I., Tomita M., Umeyama K., Urakami K.;
"New splicing pattern of the gene for procollagen C-proteinase.";
Cell Struct. Funct. 23:125-125(1998).
EMBL; AB012139; BAA75639.1; -.
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9.9%; Score 183; DB 11; Length 1012;
Best Local Similarity 44.4%; Pred. No. 7.5e-08;
Matches 48; Conservative 15; Mismatches 37; Indels 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROCOLLAGEN C-PROTEINASE 3 (FRAGMENT)
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R MEROPS; MI2.005;

R InterPro; IPR000152;

R InterPro; IPR000152;

InterPro; IPR000861;

R InterPro; IPR001881;

Pfam; PF00008; EGF; 1.

Pfam; PF00481; CUB; 2.

R PROSITE; PS0010; ASX_HYDROXYL; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01187; EGF_CA; 1.
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                                                                                                                                                               MSSP, P00742; HRG.
MGD; MGI.1346044; T112.
InterPro; IPR000130; -.
InterPro; IPR000152; -.
InterPro; IPR000551; -.
InterPro; IPR000559; -.
InterPro; IPR00059; -.
InterPro; IPR001801; -.
Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
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Search completed: September 5, 2001, 10:55:46 Job time: 103 sec

fi

Search time 20.92 Seconds (without alignments) 999.774 Million cell updates/sec US-09-457-066-43 345 1 MLLGLLLTSALAGQRTGT......DVALEHHEECDCVCRGNAGG 345 Compugen Ltd of hits satisfying chosen parameters: GenCore version 4.5 Copyright (c) 1993 - 2000 Comp 412676 seqs, 60623988 residues 5, 2001, 10:54:38 Post-processing: Listing first 45 summaries protein search, using sw model OLIGO Gapop 60.0 , Gapext 60.0 seq length: 0 seq length: 2000000000 September 0 Title: Perfect score: Scoring table: , Fotal number Word size : DB 03 OM protein Sequence: Searched: Minimum Maximum Run on:

A\_Geneseq\_0601:\*

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| SIDS8/gcgdata/geneseqgeneseqgp/AA1991.D

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Mouse zveqf3, SEO	Murine vascular en	A murine platelet-	Murine TANGO 128.	Human VEGF-X prote	Human VEGF-X prote	Human VEGF-X PDGF-	Human VEGF-X prote	Human VEGF-X prote	A fragment of plat	Lung cancer associ
	ID	AAB48658	AAY96861	AAY84559	AAB01427	AAB10631	AAB10632	AAB10642	AAB10637	AAB10638	AAY84558	AAB58438
	DB	21	21	21	21	21	21	21	21	21	21	21
	Query Match Length DB	345	345	345	180	113	113	149	227	227	318	339
øР	Query Match	100.0	100.0	100.0	27.2	15.1	15.1	15.1	15.1	15.1	15.1	15.1
	Score	345	345	345	94	52	52	52	52	52	52	52
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(first entry)

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26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c vegf4 or fragments thereof, particularly human zvegf4/human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 or fragments thereof, particularly human zvegf4 human zvegf4 cucleic acids; the recombinant expression of human zvegf4 an antibody which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells genetic zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may also be in the treatment of periodonial disease and fractures. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the human growth factor homologue zvegf4 (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/YGFF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (ABA88654) characterised by a PDGF cystine knot structure, and a CUB domain characterised by a PDGF cystine knot structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents mouse zvegf3.
                                                                                                                    factor homologs and the nucleic acids that encode them, useful
                                                                                                                                                                     e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 130-131; 143pp; English.
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N-PSDB; AAC81583.
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PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180 9 Gaps 9 1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 0 DB 21; Length 345; Indels ; 0 Query Match 100.0%; Score 345; I Best Local Similarity 100.0%; Pred. No. 0; Matches 345; Conservative 0; Mismatches 121 181 61 121 οy ò g Ω 셤 δ qq

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301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345 ò

241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300

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AAY96861 standard; Protein; 345 AA RESULT AAY96861 ID AAY9 XX

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Query Match

DB 21; Length 345;

1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60

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nurine 2VBGF3 are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY9685) and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (bpGF) family. The CUB domain shows homology to CUB domains in neuropilins, human bone morphogenetic protein-1, porcine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus laevis toroiloid-like protein. Structural analysis and homology predict that 2VBGF3 polypeptides complex with a second polypeptide to form multimeric proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3. ZVBGF3 is useful for stimulating the growth of fibroblasts or smooth muscles cells, for activating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVBGF3 useful for requiring (post-development) organ growth, regeneration and maintenance, as well as tissue maintenance and repair processes. ZVBGF3 diabetic retinopathy, ischemic limb disease, peripheral vascular diabetic retinopathy, ischemic limb disease, myccardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound healing, chronic liver disease and haemangioma formation. ZVBGF3 can also be used to modulate neurite growth and decome and for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel zveqf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising an epitope bearing portion of a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This shows a murine ZVEGF3 a novel vascular endothelial growth factor
                                                                                                                   Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
                                                                                                                                       Cysteine knot; platelet derived growth factor; PDGF; neuropilin, chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoemaker KE;
                                                                           Murine vascular endothelial growth factor homologue, ZVEGF3
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N-PSDB; AAA51527.
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21-OCT-1999;
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carcinoma

found in the lung, kidney or liver.

345 AA;

us-09-457-066-43.Sep5oli.rag

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PUGE-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and also be used to promote fibroblast mitogenesis in amamal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choricoarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma and erythroleukemia, can be identified by testing for expression of PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions,
and/or growth or motility of cells expressing a PDGF-C receptor. PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VBGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents murine platelet-derived growth factor (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation,
                                                          mll1g1111tsalaggrtgtraesnlssklq1ssdkeqngvqdprhervvtisgngsihs
                                            PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                                 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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                                                                                                                                                        LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
  Uùtela M, Alitalo K;
                                                                                                                                                                                                                                                                                 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine platelet-derived growth factor C (PDGF-C).
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Betsholz C;
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Heldin C,
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21-MAY-1999;
15-JUL-1999;
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03-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; ostboarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                           GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
                                            Gaps
                                                                                                          MILLGLILLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                      Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
  21;
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Score 345; Pred. No. 0;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB01427 standard; Protein; 180 AA.
                                            ;
0
  100.0%;
                    100.08;
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                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 129
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine TANGO 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-2000
                                            345;
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AAB10632
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                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chiseases e.g. myasthemia gravis, autoimmune diseases e.g. myasthemia gravis, autoimmune disbetes and systemic clupus erythematosus. The nucleic acids are also useful for producing cranagenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, copnostic assays, prognomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating aubject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVW 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.2%; Score 94; DB 21; Ld 100.0%; Pred. No. 5.9e-82; ive 0; Mismatches 0;
"Unidentified amino acid"
                                                                 "Unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular disorders can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 26; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10631 standard; Protein; 113
                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                        98US-0223546.
                                                                                                                                                                      99WO-US31025
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Best Local Similarity 100.
Matches 94; Conservative
 /note=
                                   'note=
                                                                     /note=
                                                                                                                                                                                                                                                                                                           WPI; 2000-465743/40.
               Misc-difference 167
                                                 Misc-difference 172
                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA47478
                                                                                                   WO200039284-A1
                                                                                                                                                                      23-DEC-1999;
                                                                                                                                                                                                        30-DEC-1998;
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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis;

Human VEGF-X protein fragment #1.

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antirhitatic, antirboriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues regeneration and organ and itssue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcars, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence reperseents the human VEGF-X protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds \mbox{-}
rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 LYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yon JR, Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; L
5.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vascular endothelial growth factor protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 52; DB 100.0%; Pred. No. 5.9 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10632 standard; Protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 127pp; English.
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                                                                                                                                                                                                                                                                                                                                       98GB-0028377.
                                                                                                                                                                                                                                                                                   99WO-US30503
                                                                                                                                                                                                                                                                                                                                                                                              99US-0164131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sprengel JJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-442669/38
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Les 52; Conserv
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                                                                                                                                                                     WO200037641-A2
                                                                                                                                                                                                                                                                                                                                    22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dhanaraj SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human VEGF-X
                                                                                                                                                                                                                                                                                21-DEC-1999;
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                                                                                                                                                                                                                            29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon RD,
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Matches
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing diseases associated with inappropriate angiogenesis activity
tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a novel vascular endothelial growth factor-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such as cancer, rheumatoid arthritis, psoriasis and wounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 LYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sprengel JJ, Yon JR, Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; I
5.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.1%; Score 52; DB 100.0%; Pred. No. 5.9
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                                                                                                                                                                                                                                                                                                                             99US-0124967.
99US-0164131.
                                                                                                                                                                                                                                                 99WO-US30503.
                                                                                                                                                                                                                                                                                                    98GB-0028377
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Best Local Similarity 100.0
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                                                                                                                                      WO200037641-A2
                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dhanaraj SN,
                                                                                                                                                                                                                                              21-DEC-1999;
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08-NOV-1999;
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                                                                                                                                                                                                                                                                                                       22-DEC-1998;
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This invention describes a novel vascular endothelial growth factor-X
(VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
vulnerary, cytostatic, antirheumatic, antiarchinic, antipsoriatic and
antidiabetic activity and acts as an anglogenesis and vascularization
cequlator. An antisense molecule of the invention is useful for treating
or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
cetinopathy by inhibiting anglogenic activity or inappropriate
vascularization including formation and proliferation of new blood
vessels, growth and development of tissues, tissue regeneration and organ
and tissue repair in a subject. The products of the invention are useful
for preparing medicaments for treating wounds such as dermal ulcers,
pressure sores, venous sores, diabetic ulcers and burns and to promote
skin graft growth, tissue repair, proliferation of new blood vessels,
tissue regeneration and organ repair by promoting anglogenic activity or
vascularization. This sequence represents a human VEGF-X protein
CDGF-like domain which can be expressed in E. coli systems and which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Yon JR, Dijkmans JJH, Gosiewska A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%; Score 52; DB 21; I
100.0%; Pred. No. 7.4e-42;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB10637 standard; Protein; 227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 24; 127pp; English
                                                                                                                                                                                                           98GB-0028377.
99US-0124967.
99US-0164131.
                                                                                                                                            99WO-US30503
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sprengel JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.1
Best Local Similarity 100.
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                               (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human VEGF-X protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442669/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA71986
WO200037641-A2.
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                                                                                                                                        21-DEC-1999;
                                                                                                                                                                                                                                                   18-MAR-1999;
08-NOV-1999;
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                                                                                                                                                                                                                  22-DEC-1998;
                                                                      29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB10637;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vascular endothelial growth factor-X
(VEGF-X) protein (Ia) and its encoding polynuclectide (IIa) which has
vulnerary, oytostatic, antirheumatic, antipsoriatic and
antidiabetic activity and acts as an angiogenesis and vascularization
regulator. An antisense molecule of the invention is useful for treating
corpreventing cancer, rheumatoid arthritis, psoriasis and diabetic
retinopathy by inhibiting angiogenic activity or inappropriate
vascularization including formation and proliferation of new blood
vessels, growth and development of tissues, tissue regeneration and organ
and tissue repair in a subject. The products of the invention are useful
for preparing medicaments for treating wounds such as dermal ulcrs,
pressure sores, venous sores, diabetic ulcers and burns and to promote
skin graft growth, tissue repair, proliferation of new blood vessels,
tissue regeneration and organ repair by promoting angiogenic activity or
vascularization. This sequence represents a human VEGF-X protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; anticheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                       New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                    Gosiewska A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 52; DB 21; Length 22 100.0%; Pred. No. 1.1e-41; ive 0; Mismatches 0; Indels
                                                                                                                                                                                   Dijkmans JJH,
                                                                                                                                                                                                                                                                                                         Disclosure; Fig 17; 127pp; English.
                                                                                                                                                                                  Sprengel JJ, Yon JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB10638 standard; Protein; 227 AA
                                                                                                                     99US-0124967.
                                                                                                           98GB-0028377.
                                                                                   99WO-US30503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100. S2; Conservative
                                                                                                                                                          (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human VEGF-X protein #3.
                                                                                                                                                                                                                    WPI; 2000-442669/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 AA;
                                                                                                                                                                                                                                  N-PSDB; AAA71981
                                   WO200037641-A2
             Homo sapiens.
                                                                                                                                                                                               Dhanaraj SN,
                                                                                  21-DEC-1999;
                                                                                                          22-DEC-1998;
                                                                                                                      18-MAR-1999;
                                                                                                                                  08-NOV-1999;
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                                                           29-JUN-2000
                                                                                                                                                                                  Gordon RD,
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Best Local 3
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AAB10638
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has validate to "Artostatic", antinheumatic. antiarchitic, antiarchitic, antiarchitic, antiarchitic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and itssue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VBCF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    Yon JR, Dijkmans JJH, Gosiewska A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 LYSCIPRNESVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 18; 127pp; English.
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                                                                                                                                                                                               98GB-0028377.
99US-0124967.
99US-0164131.
                                                                                                                                99WO-US30503
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                                                                                                                                                                                                                                                                                                                                                                                                        Sprengel JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Conservative
                                                                                                                                                                                                                                                                                                                                  (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-442669/38
                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA71982
WO200037641-A2
                                                                                                                                   21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Dhanaraj SN,
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                                                                                                                                                                                                     22-DEC-1998;
                                                                                                                                                                                                                                     18-MAR-1999;
08-NOV-1999;
                                                                 29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                    Gordon RD,
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Lung cancer associated polypeptide sequence SEQ ID 776.
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                                                                                                                                 WO200055180-A2
                                                                                                                                                                                                                                      (HUMA-) HUMAN
                                                                                                           Homo sapiens
                                                                                                                                                                                                             12-MAR-1999;
                                                                                                                                                           21-SEP-2000
                                                                                                                                                                                                                                                                             Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or growth or motility of cells expressing a PDGF-C receptor.

Doff-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The used for stimulating connective tissue or wound healing. The be used for stimulating connective tissue or wound healing. The pDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and used to induce the receptor-binding specificity of PDGF-C and used to induce two promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choricarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma and erythnoleukamia, can be identified by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions, especially found in the lung, kidney or liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human platelet-derived growth factor C (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation,
                                                                                                                                                                                                                                                                                                                                        Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 lysctprnfsvsireelkrtdtifwpgcllvkrcggncacclhncnecgcvp 271
                                                                                                                                                                                                                                                               Alitalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 318;
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                                                                                                                                                                                                                                                               Uutela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 21; I
Pred. No. 1.4e-41;
0; Mismatches 0;
                                                                                                                                                                                                                                                              Lee X, Ponten A,
Betsholz C;
                           /note= "encoded by AAS"
                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD.
Location/Qualifiers
287
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.1%; Scc.
100.0%; Pre
0; 7
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                                                                                                                                             98US-0108109.
98US-0110749.
98US-0113002.
                                                                                                        99WO-US22668
                                                                                                                                 98US-0102461
                                                                                                                                                                                   99US-0135426
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                                                                                                                                                                                                                                                              Aase K,
Heldin C,
                                                                                                                                                                                                                                                                                                   2000-292954/25
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 AA;
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA12524
               Misc-difference
                                                      WO200018212-A2
                                                                                                       30-SEP-1999;
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                                                                                                                                                                                                                                                          Eriksson U,
                                                                                                                                                         03-DEC-1998;
18-DEC-1998;
                                                                                                                                                                                 21-MAY-1999
15-JUL-1999
                                                                               06-APR-2000
                                                                                                                                30-SEP-1998
                                                                                                                                               12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
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ID AAB5
XX
AC AAB5
XX
DT 14-M
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                                 cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nepirotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; prolliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425. AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrohitestinal general; rephrotropic; antibifective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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cancer associated protein; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 1305-1306; 1425pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           such as lung cancer
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROSE/) ROSEN C A.
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Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.

Homo sapiens.

Human PRO200 protein sequence.

(first entry)

07-DEC-1999

AAY41766;

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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has candothelial cell growth factor-E (VEGF-E) polypeptide which has transpectably, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans; It is useful in wound repair and tissue generation and may especially be used to treat cardiac hypertrophy of It can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), vascular disease, or neovascularization associated with tumor formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding tissue samples They can also be used to diagnose a disease or respectably by the disease related form of VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by camely or the mammals and the conding sequence isolated from a candon conding and candons used it candons and and a top or the angiogenic disorder such as a tumor), by capan also he used to cardiovascular to a disease related to a mutated form of solated from a second or candons and the candons and the candons and a top or candons and the cando
                                                 tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene mapping. This sequence represents the human VEGF-E in the method of the invention.
VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy;
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98US-0184216.
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                                                                                                                                      15.1%; Score 52; DB 20; Length 345; 100.0%; Pred. No. 1.5e-41; ive 0; Mismatches 0; Indels
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Best Local Similarity 100. Matches 52; Conservative

ð 셤 RESULT 13 AAY41766 ID AAY4

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Query Match

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98US-0081195.
98US-0081203.
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growth factor related protein; VEGF-R protein;

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related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that untagonise its activity. VEGF-R antiagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting tissue growth. This is useful for inhibiting tumour growth and for treating cancer. VEGF-R itself can be used to stimulate tissue growth, angiogenesis and to traat coronary artery blockage. The VEGF-R coding sequence can be used for the recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a vascular endothelial growth factor
                                                                                                                                                                                             tissue growth inhibition; tumour growth; cancer; tissue growth; angiogenesis; coronary artery blockage.
                                                                                                                              Human vascular endothelial growth factor related protein.
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AAY30023 standard; Protein; 345 AA.
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                                                                                                                                                                         Vascular endothelial
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular
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growth factor related protein and related for identifying antagonists and binding

98US-0098548. 98US-0072635. 98US-0088089. 98US-0090544.

Song HY; & CO ELI.

Na S,

99WO-US01574

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Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;
CUB domain; PDGF-like activity; mitogenic; osteogenic;
neovascularisation; tissue repair; proliferation; differentiation;
                                 Gaps
                              ;
0
                                                                          247 LYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP 298
Length 345;
                              0; Indels
                Pred. No. 1.5e-41;
15.1%; Score 52; DB 20;
100.0%; Pred. No. 1.5e-41;
tive 0; Mismatches 0;
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                                                                                                                                                                 AAB48657 standard; Protein; 345
                                                                                                                                                                                                                                                       Human zvegf3, SEQ ID NO:33.
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                               Conservative
   Query Match
Best Local Similarity
                                                                                                                                                                                                                          09-MAR-2001
                               52;
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                                                                                                                                     RESULT 15
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1.5e-41; hes 0;

Query Match 15.1%; Score 52; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 52; Conservative 0; Mismatches

Length 345;

DB 20;

247 lysctprnfsvsireelkrtdtifwpgcllvkrcggncacclhncnecqcvp 298

247 LYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP

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345 AA;

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Treatment or repair of particularly human zvegf4/human zvegf4 or itsagments thereof, particularly human zvegf4/human zvegf4 or itsagments thereof; particularly human zvegf4/human zvegf4 cucleic acids; the recombinant expression of human zvegf4, an antibody which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or method of modulating the proliferation, differentiation or method of modulating the proliferation, differentiation or zvegf4-derived polypeptides; and a method of detecting a genetic ragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of labelmer's disease or multiple sclerosis). Due to their osteogenic activity, they may also be used in the treatment of periodontal disease and fractures. They may also be used to their osteogenic activity, they may also be used to their osteogenic activity, they may also be used to their osteogenic activity, they may also be used to their osteogenic activity, they may also be used to the chance expansion and mobilisation of haemactopoietic stem cells and endothelial precursor stem cells, which may be used to treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf3.
liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia; immunomodulation; hepatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4.is a member of the PDGF (platelet-derived growth factor)/VBGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (AAB48654) characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor homologs and the nucleic acids that encode them, useful e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the human growth factor homologue zvegf4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilbertson DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 48; Page 125-126; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheppard PO,
                                                                                                                                                                                                                                                                                                          03-MAY-1999; 99US-0304216.
10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
                                                                                                                                                                                                                                                            03-MAY-2000; 2000WO-US40047
                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilbert T, Hart CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-687541/67
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                                                                                                                                                       WO200066736-A1
                                                                                                       Homo sapiens.
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Ouery Match 15.1%; Score 52; DB 21; Length 345; Best Local Similarity 100.0%; Pred. No. 1.5e-41; Matches 52; Conservative 0; Mismatches 0; Indels

tches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 247 LYSCTPRNFSVSIREELKRIDIFWPGCLLVKRCGGNCACCLHNCNECQCVP 298

Qy Db

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Search completed: September 5, 2001, 10:56:31 Job time: 113 sec

Run

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RESULT 2
US-09-108-140-6
Sequence 6, Application US/09208140
Sequence 6, Application US/09208140
Sequence 6, Application US/09208140
GENERAL INFORMATION:
TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
TITLE OF INVENTION: AND METHODS THEREOF TO IDENTIFY ANTIVIRAL COMPOUNDS
FILE REFERENCE: P50743
CURRENT APPLICATION NUMBER: US/09/208,140
CURRENT FILING DATE: 1998-12-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
FIRMATH. A.A.
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APPLICANT: Del Vecchio, Alfred
TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
TITLE OF INVENTION: AND METHODS THEREOF TO IDENTIFY ANTIVIRAL COMPOUNDS
FILE REFERENCE: P50743
CURRENT APPLICATION NUMBER: US/09/208,140
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5.
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                                     US-07-690-192-2
US-08-487-550-2
US-08-88-12-586-16
US-08-487-550-6
US-08-487-550-6
US-08-487-550-6
US-08-078-311-14
US-08-078-311-24
US-08-078-311-24
US-08-078-311-24
US-08-078-311-24
US-08-078-311-24
US-08-078-311-24
US-08-078-311-24
US-08-078-311-24
US-08-09-092-14
US-08-460-402-14
US-08-460-402-14
US-08-460-402-14
US-08-408-969-17
US-08-092-270-2
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100.0%; Pred. No.
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100.0%; Pic
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Best_Local Similarity
Matches 8; Conserv
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; ORGANISM: Viral
US-09-208-140-5
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Patent No. 5338678
Patent No. 5338678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 3, App
Sequence 9, App
Sequence 22, App
Sequence 22, App
Sequence 22, App
Sequence 185, Sequence 185, Sequence 185, Sequence 185, Sequence 185, Sequence 185, Sequence 14, App Sequence 1
                                                                                                                                                                                                                                                                                              MLLLGLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345
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Seguence 4, 1
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Sequence 3,
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Sequence 1
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.: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-938-365-3
US-08-749-169A-3
US-08-130-032A-3
US-08-10-032A-3
US-08-10-10-9
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-01B-22
US-08-957-01B-22
US-08-957-01B-2
US-08-096-762-185
US-08-096-762-185
US-08-096-762-185
US-08-096-762-185
US-08-468-671-14
US-08-468-671-14
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US-08-460-402-4
US-08-855-825-12
US-08-855-825-14.
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Match Length
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Maximum DB :
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Meiklejohn, Ph.D., Anita L.
             ADDRESSEE:
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                                                                                COUNTRY:
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                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yang, Pan
TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%; Score 8; DB 1;
100.0%; Pred. No. 19;
ive 0; Mismatches
            Pred. No. 1.8;
                              Mismatches
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8389-031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
100.0%; Pre
                                                                                                                                                                                                                         APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
APPLICANT: Sieron, Aleksander
APPLICANT: Brenner, Mitch
TITLE OF INVENTION: RECOMBINANT
TITLE OF INVENTION: DRUG DEVELOI
                                                                                                                                                                             Sequence 1, Application US/08572225 Patent No. 5807981
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Patent No. 5989909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amire
            Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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APPLICANT: Yang, 1
                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1:
CLASSIFICATION:
                                                                              30 LLLGLLLL 37
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US-08-938-365-3
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; Patent No. 5989909
; GENERAL INFORMATION:
APPLICANT: Yang, Pan
TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
; CITY: Boston
                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,365
FILING DATE: 26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 1BM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                              09404/040001
                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 094C
TELECOMMUNICATION INFORMATION:
TELEFAN: 617/542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-1997
N: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 855 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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225 Franklin
                                                                                                                                                                                                                          FILING DATE: 26-SEP-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                    ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LLLGLLLL 14
                     Boston
                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LLLGLLLL 9
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12 LLIGLLLL 19
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                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02140
                                                                              US-09-130-032A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-07-925-695-5
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                                                                                                                                                                                                                                                                                                               Length 867;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,169A
                                                                                                                                                                                                                                                                                                           2.3%; Score 8; DB 2
100.0%; Pred. No. 21;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAVALLIE, Edward
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/040001
TELECOMMUNICATION:
TELEPHONE: 617/542-5070
TELEFRA: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08749169A Patent No. 5846770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERRICE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,618
                                                                            TELEFAX: 617/542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100...
                                                                                                                                                                                             ; TOPOLOGY: linear
, MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-938-365-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-749-169A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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US-08-749-169A-3
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NON'A, NON'B HEPATITIS VIRUS GENOME, POLYNUCLEOTIDES, POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND DETECTION SYSTEMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young STREET: 1850 M Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,032A
FILING DATE: August 4, 1998
CLASSIFICATION: 530
                                                              APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Recie, Lisa
APPLICANT: DeRobertis, Edward
TITLE OF INVENTION: HUMAN CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3%; 5cc.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284-DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/07925695
Patent No. 5428145
GENERAL INFORMATION:
APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NKAMUTA, Tetsuo
TITLE OF INVENTION: NON-A, NON-B H
TITLE OF INVENTION: DETECTION SYST
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, DeGrandi,
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 3, Application US/09130032A Patent No. 5986056 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 954 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.،
اتات 8; Conservative
                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                               CITY: Cambridge
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Length 954; Indels

2.3%; Score 8; DB 2;

Query Match 2.3%; Score 8; DB 2 Best Local Similarity 100.0%; Pred. No. 22; Matches 8; Conservative 0; Mismatches

2 LLLGLLLL 9

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FILING DATE: 14-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-078-311-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minneapolis
                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18 CLASSIFICATION:
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APPLICANT:
APPLICANT:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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Vigon, Isabelle
Wendling, Francoise
WENTION: Polypeptide of a Growth Factor Receptor
VENTION: Family, Application in the Diagnosis and Treatment of
VENTION: Myeloproliferative Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/925,695
FILING DATE: 19920807
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: JP 287402/91
FILING DATE: 09-AUG-1991
PRIOR APPLICATION NUMBER: JP 360441/91
FILING DATE: O5-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 06/87-480
TELECOMMUNICATION INFORMATION:
TELERONOCKET NUMBER: 06/87-480
TELEX: WUI 64470
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: SANT AND ACTORNATION:
TELEX: WUI 64470
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charon, Martine
Gisselbrecht, Silvie
Penciolelli, Jean-Francios
Souyri, Michele
Tambourin, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-078-311-9; Sequence 9, Application US/08078311; Patent No. 5925750
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: POLYTITLE OF INVENTION: Family TITLE OF INVENTION: Myel NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Charon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3014 LLLGLLLL 3021
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US-07-925-695-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
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90 South 7th Street, 3100 No. 5989833west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 2.0%; Score 7; DB 2;
100.0%; Pred. No. 7.4;
iive 0; Mismatches
APPLICATION NUMBER: WO PCT/FR90/00762 FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: KOWALCHYK, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 14-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charon, Martine
Gisselbrecht, Silvie
Penciolelli, Jean-Francios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFFCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/460,402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/08460402; Patent No. 5989833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wendling, Francoise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Souyri, Michele
Tambourin, Pierre
Varlet, Paule
Vigon, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                         612-332-5300
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                      TELEPHONE: 612-332-530
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.0
Best Local Similarity 100.
Matches 7; Conservative
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Gaps
                                                                                                                                                                                                              APPLICANT: Madaio, Milliam V.
APPLICANT: Madaio, Michael
APPLICANT: Madaio, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US 60/029,592
23-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UPN-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,001
FILING DATE: 23-0CT-1997
APPLICATION NUMBER: US 60/029,595
FILING DATE: 23-0CT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08341219
Patent No. 5643877
GENERAL INFORMATION:
APPLICANT: Zohar, Y.
                                                                                                                                                              ; Sequence 22, Application US/09496301
; Patent No. 6248565
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.0
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-09-496-301-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gothilf, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                               LIGITIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               19103
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                                                                                                                                           US-09-496-301-22
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APPLICANT:
APPLICANT:
APPLICANT:
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One Liberty Place, 46th floor
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                                                                                                                                                                                                                                                                                                        Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%; Score 7; DB 4
100.0%; Pred. No. 8.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,001B
FILING DATE: 23-CCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 60/029,592
FILING DATE: 23-CCT-1996
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                             8076.840503
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APPLICANT: Madaio, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08957001B Patent No. 6228621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: windows
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.03
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                  TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-460-402-9
                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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US-08-957-001B-22
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GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
                                                                                                                                                         NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 3074
REFERENCE/DOCKET NUMBER: 8399-003-999
TELECOMNUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%; Score 7;
  US/08/912,314A
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18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 185, Application US/08053131 Patent No. 5661016
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/341,219
FILING DATE: 05-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Smith, William M. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                           not relevant
                30-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               LENGTH: 85 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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California
  APPLICATION NUMBER:
FILING DATE: 30-JUN
                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: NO US-08-912-314A-22
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STREET: On
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APPLICANT: Rivier, J.
APPLICANT: Rivier, J.
APPLICANT: Powell, J.
APPLICANT: Sherwood, N.
APPLICANT: Gothilf, Y.
TITLE OF INVENTION: Compounds and Methods For Controlling
TITLE OF INVENTION: Reproduction in Fish
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
Compounds and Methods For Controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 85;
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #10, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,219
FILING DATE: 05-DEC-1994
ATTONENT AGENT INFORMATION:
NAME: COLUZZI, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/POCKET UNBER: 8399-003-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100-0209
TELECOMMUNICATION 100-0209
TELECOMMATION FOR SEQ ID NO: 22:
SEQUENCE CHRARCTERISTICS:
LENGTH: 85 mino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                         Reproduction in Fish
                                       NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-912-314A-22
; Sequence 22, Application US/08912314A
; Eatent No. 6210927
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P.
Matches 7; Conservative 0;
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MEDIUM TYPE: Floppy
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-341-219-22
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEPRA: 415-326-2400
; TELEPRA: 415-326-2402
; INFORMATION FOR SEO ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENOTH: 116 amino acids
; TVPE: amino acid
; TVPE: amino acid
; TVPE: protein
US-08-053-131-185

QUETY MATCh

QUETY MATCh

QUETY MATCh

QUETY MATCh

Best Local Similarity 100.0%; Pred. No. 33;
MATChes 7; Conservative 0; Mismatches 0; Indels
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Search completed: September 5, 2001, 10:56:51 Job time: 113 sec

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                                                                                                                                                                       RESULT 1
CPS1_HUMAN
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                                                             ; Search time 12.76 Seconds (without alignments) 926.187 Million cell updates/sec
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sapien
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haplochromi
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canine aden
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sus scrofa
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schizosacch
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                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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P08686; P04033; Q01204;
01-NOV-1986 (Rel. 03, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
CYTOCHROME P450 XXIB (EC 1.14.99.10) (STEROID 21-HYDROXYLASE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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CYP21A2 OR CYP21B OR CYP21.
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MEDLINE-99335263; PubMed-10408778;
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MEDLINE-98180883; PubMed-9580109;
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    VARIANTS CAH ASN-172; ASN-236; LE
MEDLINE=95268421; PubMed=7749410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. THIS INVOLVED IN AN UPON P. NITROANISOLE, ANILINE, D-BENZPHETAMINE, DELTA(9)-
TETRAHYDROCANNABINOL (THC) AND STRYCHNINE.
CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
OXIDIZED FLAVOPROTEIN + H(2)0.
SUBCELLULAR LOCATION: MEBRANE-BOUND. ENDOPLASMIC RETICULUM.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification of a cytochrome P450 isozyme belonging to a subfamily of P450 IIB from liver microsomes of guinea pigs."; Biochem. Biophys. Res. Commun. 172:607-613(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum. NoN_TER 20\, 20\,
                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTCCHROME P450IIB (EC 1.14.14.1) (FRACMENT).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-HARTLEY; TISSUE-Liver;
MEDLINE-91054472; PubMed-2173574;
Marimatsu S., Akutsu Y., Matsunaga T., Watanabe K., Yamamoto I.,
Yoshimura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                            Length 494;
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                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%; Score 8; DB 1; Length 20; 100.0%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA; 2259 MW; 78DC81280C970A55 CRC64;
                                                                                       0;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PLATELET FACTOR 4 PRECURSOR (PF-4).
SCYB4 OR PF4.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                20 AA
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                        2.6%; Score 9; DB 1
100.0%; Pred. No. 0.4
iive 0; Mismatches
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0; Mismatches
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                     Query Match 2.6
Best Local Similarity 100.
Matches 9; Conservative
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InterPro; IPR001128;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10141;
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                                                                                                                                                  1 MLLLGLLLL 9
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P34033;
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P06765;
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PLF4_RAT
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                                                                                                                                                                                                                                                                                                                                Spectrometry.";
Eur. J. Biochem. 223:203-210(1994).

Eur. J. Biochem. 223:203-210(1994).

Eur. J. Biochem. 223:203-210(1994).

FUNCTION: PLATELET FACTOR 4, NONCOVALENTLY BOUND TO A PROTEOGLYCAN MOLECULE, IS RELEASED DURING PLATELET AGGREGATION. PF4 NEUTRALIZES THE ANTICOAGULANT EFFECT OF HEPARIN BECAUSE IT BINDS MORE STRONGLY TO HEPARIN THAN TO THE CHONDROITIN-4-SULFATE CHAINS OF THE CARRIER MOLECULE. CHEMOTACTIC FOR NEUTROPHILS AND MONOCYTES.

SUBUNIT: HOMOTETRAMER.

SUBUNIT: HOMOTETRAMER.

HOMOTETRA OF GAL-GALNAC DISACCHARIDE WHICH IS MODIFIED WITH SIALIC ACID RESIDUES (MACROHETEROGENEITY).

SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                Ravanat C., Gachet C., Herbert J.-M., Schuhler S., Guillemot J.-C., Uzablaga F., Ploard C., Ferrara P., Freund M., Cazenave J.-F., Hat platelets contain glycosylated and non-glycosylated forms of platelet factor 4. Identification and characterization by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (CE4) (EPIDIDYMAL SECRETORY PROTEIN E4).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00048; IL8; 1.
PRINTS; PR00437; SMALLCYTKCXC.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
CYtokine; Platelet; Proteoglycan; Heparin-binding; Chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Doi T., Greenberg S.M., Rosenberg R.D.; "Structure of the rat platelet factor 4 gene: a marker for megakaryocyte differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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D9CCAD2B6A284496 CRC64;
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8; I
Pred. No.
                                                                                                                                                     O-GLYCOSYLATION.
MEDLINE-94307262; PubMed-8033893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.3%; Sco.
100.0%; Pre
0;
                                                              megakaryocyte differentiation.";
Mol. Cell. Biol. 7:898-904(1987)
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87 B
31 O
11286 MW;
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InterPro; IPR001089; -.
InterPro; IPR001811; -.
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2 LLLGLLLL 9
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SEQUENCE 47
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                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CLL;
                                                                                                                                                                                                                                                                        PEN3_ADECC
Q65950;
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SEQUENCE
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                                                                                                                                                                                                                                                       RESULT 6
PEN3_ADECC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NRRL Y-5445;
MEDLINE=95028149; PubMed=7941737;
Agaphonov M.O., Poznyakovski A.I., Bogdanova A.I., Ter-Avanesyan M.D.;
"Isolation and characterization of the LEU2 gene of Hansenula
                                                                                    Gaps
                TISSUE=Epididymis;
MEDINE=95263175; PubMed=7744511;
Ellerbrock K., Pera I., Hartung S., Ivell R.;
"Gene expression in the dog epididymis: a model for human epididymal
function.";
                                                                                                                                                                                                                                                                                                                                      MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
15AAF315BA13958C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN IN LEUZ 3'REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                       Pfam; PF00095; wap; 2.
PRINTS; PR00003; 4DISULPHCORE.
PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
                                                                                                                                                                                                                                                                                                                                                        WAP .2
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                                                                                                                                                                                                                                                                                                                                                                                            2.3%; SCC_
100.0%; Pre
0;
                                                              Int. J. Androl. 17:314-323(1994)
                                                                                                                                                                                                                                                                                                                                                                         12951 MW;
                                                                                                                                                                                                                                                                      EMBL; S77395; AAB34264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymorpha.";
Yeast 10:509~513(1994).
                                                                                                                                                                                                                                                                                IPR002221;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                    Signal; Glycoprotein
                                                                               TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                        124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LLLGLLLL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4905;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ULLGLLLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLU2_PICAN
P34735;
                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                             IGNAL
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLU2_PICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine adenovirus type 1 (strain CLL), and Canine adenovirus type 1 (strain R1261). Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.NCBI_TaxID=69150, 69151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PENTON PROTEIN (VIRION COMPONENT III) (PENTON BASE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                           38575 MW; 4E955FFF5D191750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 AA; 53464 MW; B9FDF37407D0FDA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morrison M.D., Onions D.E., Nicolson L.; "Complete DNA sequence of canine adenovirus type 1."; J. Gen. Virol. 78:873-878(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3%; Scor.
100.0%; Pred. No. 3..,
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100.0%; Pred. No. 4.3
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8; Db
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Pfam; PF01686; Adeno_Penton_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97275900; PubMed-9129661;
                                                                                                                                                                                                                               EMBL; U00889; AAA19110.1; -.
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                                                                                                                                                                                                                                                   PIR; S43455; S43455.
InterPro; IPR002889; -
Pfam; PF01822; WSC; 1.
Hypothetical protein.
DOMAIN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.3
Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           373 AA;
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TISSUE=Skin;
                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                               DISULFID
                    ACT_SITE
                                                      DISULFID
                                                                                     CARBOHYD
           METAL
                                           METAL
                                                                                                                                                                                                                                                                                     BMP1_HUMAN
δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                  Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;

"Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein-1 during early embryonic development.";

Gene 134:257-261(1993).

-I- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER DIFFERENTATION OF DEVELOPING ORGANS.

-I- SURLERNIATION OF DEVELOPING ORGANS.

-I- SIMILARITY: CONTAINS 3 CUB DOMAINS.

-I- SIMILARITY: CONTAINS 3 CUB DOMAINS.

-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI2A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BONE MORPHOGENETIC PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METALLOPROTEASE
                                                                                     707 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO0480; ASTACIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS01180; CUB; 3.
                                                                                                                                                                                                                                TISSUE=Embryo;
MEDLINE=94085787; PubMed=8262384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L12249; AAA16313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 3.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000130; ...
InterPro; IPR000152; ...
InterPro; IPR000561; ...
InterPro; IPR000569; ...
InterPro; IPR001506; ...
InterPro; IPR001891; ...
                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
284
397
5509
                                                                                                                                                                                 Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1APO.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
           183 LDLLNNAV 190
                               163 LDLLNNAV 170
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84
285
398
510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
                                                                                    BMP1_XENLA P98070;
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                                                                RESULT 7
BMP1_XENLA
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Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.; "Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1."; J. Mol. Med. 76:141-146(1998).
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"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
are encoded by alternatively spliced transcripts which are
differentially expressed in some tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The C-proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BMP1_HUMAN STANDARD; PRT; 986 AA.
P13497, Q13292; Q99421; Q99422; Q99423; Q14874;
01-071-070 (Rel. 13, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last noncation update)
01-0CT-2000 (Rel. 40, Last sequence update)
                                                                                             BY SIMILARITY.
BY SIMILARITY.
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N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                  SIMILARITY). SIMILARITY).
                         (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                        Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (Po
1B6980D716DC9B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Novel regulators of bone formation: molecular clones activities.";
                                                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
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                                                               ZINC (CATALYTIC) ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                        DB 1;
5. 6.1;
                                                                                                                                                                                                                                                                                                                                        2.3%; Scc.
100.0%; Pred. No. v
0; Mismatches
                      ZINC (CATALYT
BY SIMILARITY
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                                                                                                                                                                                                                                                                                          80673 MW;
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1176
1177
1180
1186
552
550
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1105
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562
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                                                                                                                               522
537
62
105
295
326
562
707 AA;
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554
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177
180
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2 LLLGLLLL
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P98063;
                                                    DISULFID
            DISULFID
                                                                        DISULFID
                                                                                            CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                                                                                                VARSPLIC
VARSPLIC
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VARSPLIC
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CONFLICT
CONFLICT
                                DISULFID
                                            DISULFID
                                                                                                                                     CARBOHYD
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                                                                                                                                             VARSPLIC
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             ΙΙ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUB 1.
CUB 2.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
Biol. Chem. 269:32572-32578(1994).
- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II INDUCES CARTILAGE AND BONE FORMATION.
- CATALYTIC ACTIVITY. ELEAVED OF THE C-TERMINAL PROPEPTIDE AT ALA-I-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-I-ASP IN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUB 3.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
                                                                                           ALTERNATIVE PRODUCTS: 6 ISOFORMS; BMP1-1, BMP1-2, BMP1-3 (SHOWN HERE), BMP1-4, BMP1-5 AND BMP1-6; ARE PRODUCED BY ALTERNATIVE
                                                                   ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
                                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPR001805; ...
R InterPro; IPR001801; ...
R Pfam; PF01400; Astacin; 1.
R Pfam; PF00431; CUB; 5.
R Pfam; PF00431; CUB; 5.
R PRIMTS; PR00480; ASTACIN.
R PROSITE; PS00142; ZINC_PROTEASE; 1.
R PROSITE; PS001010; ASX_HYDROXYL; 2.
R PROSITE; PS001010; ASX_HYDROXYL; 2.
R PROSITE; PS001010; ASX_HYDROXYL; 2.
R PROSITE; PS001187; EGF_2; 2.
R PROSITE; PS01187; EGF_2; 2.
R PROSITE; PS01187; EGF_CA; 2.
R Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; W Glycoprotease; EGF_like domain; Zinc; Calcium; Signal; Glycoprotein; Zymogen; Alternative_splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NC (CATALYTIC) (BY SIMILARITY). SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                      TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY
(BY
                                                            COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY)
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INC (CATALYTIC) (
SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                  EMBL; U50330; AAA93462.1; -.
                                                                                                                                                                                                                                                                            M22488; AAA51833.1; -. Y08723; CAA69973.1; -.
                                                                                                                                                                                                                                                                                               EMBL; Y08724; CAA69974.1; --
EMBL; Y08725; CAA69975.1; --
EMBL; L35279; AAC41710.1; --
PIR; A37278; A37278.
HSSP; P00736; 1APO.
MEROPS; M12.005; --
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000130; -.
InterPro; IPR000152; -.
InterPro; IPR000561; -.
InterPro; IPR000859; -.
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986
3321
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217
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                                                                                                                SPLICING
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IVPKYEVNGVKPPIGQR -> VLHSSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                                                                                                    -> GCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
which is related to the Drosophila dorsoventral gene tolloid and
encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).
-!-FONCTION: CLEAVES THE C-PERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
AND II. INDUCES CAPTILAGE AND BONE FORMATION.
-!-CATALYTIC ACTIVITY: CLEAVAGE OF THE C-TERMINAL PROPEPTIDE AT
ALA-|-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-|-ASP IN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.19) (BMP-1)
(PROCOLLAGEN C-PROTEINASE) (PCP) (MAMMALIAN TOLLOID PROTEIN) (MTLD).
                                                                                                                                                                                                                                                                                                                                                                                                                 DKDECSKDNGGCQQD -> GGELFGLLGHPPRRP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                   (IN ISOFORM BMP1-4).
MISSING (IN ISOFORM BMP1-4).
AACGGELTKLNGSITSGEWPKRYPPNKNOIWOLV -
DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 986;
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MISSING (IN ISOFORM BMP1-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN ISOFORM BMP1-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F89201913AC3CBEA CRC64;
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R -> S (IN REF. 4).
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                                                                           SIMILARITY.
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                                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING
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MEDLINE-94229342; PubMed-8174772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111248 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                  986
622
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717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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748
934
7299
703332
7033
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991 AA; 111607 MW; 68A1847783A0BB9E CRC64;
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                                                         Query Match
Best Local Similarity
                                                                                                                                                   104 CKYDFVEV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snodgrass H.R.;
     SEQUENCE
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MERK_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                             Matches
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                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
ENDOPEPTIDASE ENHANCER PROTEIN.

TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDUUM
AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING
MEMBRANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS
OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
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CUB 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; 1PR000859; -.

R InterPro; 1PR001506; -.

R InterPro; 1PR001506; -.

R InterPro; 1PR001506; -.

R Pfam; PF00431; CUB; 5.

R Pfam; PF00008; BGF; 2.

R PRIMTS; PR00048; AINC_PROTEASE; 1.

R PROSITE; PS001180; CUB; 5.

R PROSITE; PS001180; CUB; 5.

R PROSITE; PS001180; CUB; 5.

R PROSITE; PS01180; EGF_1; FALSE_NEG

R PROSITE; PS01187; EGF_2; 2.

R PROSITE; PS01187; EGF_2; 2.

R PROSITE; PS01187; EGF_1; FALSE_NEG

R PROSITE; PS01187; EGF_1; FALSE_NEG

R PROSITE; PS01187; EGF_1; FALSE_NEG

R GROWTh factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase;

M Metalloprotease; EGF_1ike domain; Zinc; Calcium; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
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(BY
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ZINC (CATALYTIC) (
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                               EMBL; L24755; AAA37306.1; -
                                                                                                                                                                                                                                                                                                                                                                 MEROPS; M12.005; -.
MGD; MGI:88176; Bmp1.
InterPro; IPRO00130; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402
466
515
577
592
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000152; -
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000561; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Zymogen
                                                                                                                                                                                                                                                                                                                                                  1APO.
                                                                                                                                                                                                                                                                                                                                                  P00736;
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                                                                     <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CD-1; TISSUE=Testis;
Dowds C.A., Burks D.J., Saling P.M.;
M. CDNA encoding part of a novel putative receptor tyrosine kinase.";
Submitted (JAN-1996) to the EMBL/Genbank/DDBJ databases.
-: CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYROSINE PHOSPHATE.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

-!- TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED PREDOMINANTLY IF NOT

EXCLUSIVELY IN THE MONOCYTIC LINEAGE.

-!- DEVELOPMENTAL STAGE: EXPRESSED DURING MOST, IF NOT ALL, STAGES OF

EMBRYOLOGICAL DEVELOPMENT BEGINNING IN THE MORULA AND BLASTOCYST

AND PROGRESSING THROUGH THE YOLK SAC AND FETAL LIVER STAGES.

-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE MER PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and developmental expression analysis of the murine c-mer tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Graham D.K., Bowman G.W., Dawson T.L., Stanford W.L., Earp H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AXL/UFO SUBFAMILY.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                     0;
Length 991;
                                                                     0; Indels
Score 8; DB 1;
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                           994 AA
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (C-MER) (RECEPTOR TYROSINE KINASE MERTK).
      Score 8;
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Spleen;
MEDLINE=95303502; PubMed=7784083;
                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                    MERK_MOUSE STANDARD; I 060805; 062194; 01-027-2000 (Rel. 40, Created) 01-027-2000 (Rel. 40, Last sequil-027-2000 (Rel. 40, Last ann
   2.3%; 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 472-994 FROM N.A.
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EMBL; L11625; AAA85355.1;
                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001245; -.
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InterPro; IPR003006; -.
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Pfam; PF00047; ig; 2.
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InterPro; IPR000719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
                                                  -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
            Hum. Mol. Genet. 9:645-651(2000).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
                                                                                                (POTENTIAL)
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_LYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal; Repeat; Immunoglobulin domain; Proto-oncogene.

I 18 POTENTIAL.
SIGNAL
                                                                                    -! - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES
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ATP (BY SIMILARITY)
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BY SIMILARITY.
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N-LINKED (GLCN)
N-LINKED (GLCN)
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      dystrophic RCS rat.";
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Best Local Similarity
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                  PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=RCS;
MEDLINE=20164303; PubMed=10699188;
MEDLINE=20164303; PubMed=10699188;
LaVerl P.M., Yasumura D., Weir J., Matthes M.T., Abderrahim H.,
LaVail M.M., Vollrath D.;
"Mutation of the receptor tyrosine kinase gene Mertk in the retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PROTO-0COGENE TYROSINE-PROTEIN KINASE MER PRECURSOR (EC 2.7.1.112)
(C-MER) (RECEPTOR TYROSINE KINASE MERTK).
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal; Repeat;
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I -> V (IN REF. 2).

603C09FA11F76FE0 CRC64;
                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                              CYTOPIASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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100.0%; Pred. No. 8.2;
iive 0; Mismatches
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                                                            Immunoglobulin domain; Proto-oncogene.
SIGNAL 1 18 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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P57097;
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Gaps

624 LLLGLLLL 631

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                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: PÉMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                           FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION.
         01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
DESMOGLEIN 3 PRECURSOR (130 KDA PEMPHIGUS VULGARIS ANTIGEN) (PVA).
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
                                                                                                                                                                              MEDIINE=92069753; PubMed=1720352;
Amagai M., Klaus-Kovtun V., Stanley J.R.;
"Autoantibodies against a novel epithelial cadherin in pemphigus
                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, ESOPHAGUS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. ) (POTENTIAL)
LINKED (GLCNAC. .) (POTENTIAL)
60479DD46AC219A1 CRC64;
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CADHERIN 4.
DESMOGLEIN REPEAT 1.
DESMOGLEIN REPEAT 2.
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                                                                                                                                                                                                                              vulgaris, a disease of cell adhesion.";
Cell 67:869-877(1991).
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268
383
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                                                                                       Homo sapiens (Human)
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999 AA;
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MIM; 169615; -.
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92044440; PubMed=1658196; Okamoto H., Okada S.-I., Sugiyama Y., Kurai K., Lizuka H., Machida A., Miyakawa Y., Mayumi M.; Machida A., Miyakawa Y., Mayumi M.; Mucleotide sequence of the genomic RNA of hepatitis C virus isolated from a human carrier: comparison with reported isolates for conserved
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                                                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 28) Last annotation update)
6ENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN) (P22);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease.
                                                                                                                                           ENVELOPE GIKCOPROTEIN EL (GP32) (GP35); ENVELOPE GIKCOPROTEIN) (F22) (GP69) (GP70) (NS1); PROTEIN P7; NONSTRUCTURAL PROTEIN NS2 (P21) (EC 3.4.22.-); PROTEIN P7; NONSTRUCTURAL PROTEIN NS2 (P21) (EC 3.4.21.-); PROTEIN NS4 (P4); NONSTRUCTURAL PROTEIN NS4B (P27); NONSTRUCTURAL PROTEIN NS5A (P56); NONSTRUCTURAL PROTEIN NS5B (P66) (P70) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48)].

Whenellis C virus (isolate HC-16) (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and divergent regions.";
J. Gen. Virol. 72:2697-2704(1991).
-!-FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHOBIC. SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
-!-SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
                                      3033 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D00944; BAA00792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PP01560; HCV_NS1; 1.
PP01538; HCV_NS2; 1.
PP01006; HCV_NS4a; 1.
PP01001; HCV_NS4b; 1.
PP01506; HCV_NS5a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCV_capsid;
HCV_core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCV_env; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV_RdRP;
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002522; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002519;
InterPro; IPR002521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000745;
InterPro; IPR001490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JQ1303; JQ1303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P27958; IHEI.
MEROPS; S29.001; -.
MEROPS; U39.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00253]
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF01001, H
Pfam, PF01506, H
Pfam, PF00998, H
Pfam, PF01543, H
Pfam, PF01543, H
Pfam, PF01539, H
                                                                                                                                                                                                                                                                                                      Hepacivirus
                                      POLG_HCVJ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
RESULT 13
POLG_HCVJ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
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Gaps

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Mismatches

Length 999; Indels

DB 1;

Pred. No.

Query Match 2.3%; Sc Best Local Similarity 100.0%; P Matches 8; Conservative 0;

Score 8;

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                                                                                                                             NONSTRUCTURAL PROTEIN NS4A (POTENTIAL)
NONSTRUCTURAL PROTEIN NS4B (POTENTIAL)
                            CAPSID PROTEIN ( POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE/HELICASE NS3 (POTENTIAL).
                                                                                                                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
 REMOVED FROM CAPSID PROTEIN C BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MEDLINE-94151343; PubMed-8108425;
White S.A., Bond C.T., Francis R.C., Kasten T.L., Fernald R.D.,
Adelman J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL)
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P37044; P20408;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GONADOLIBERIN II PRECURSOR (GONADOTROPIN-RELEASING HORMONE II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A second gene for gonadotropin-releasing hormone: cDNA expression pattern in the brain.", Proc. Natl. Acad. Sci. U.S.A. 91:1423-1427(1994).
                                                                                                                                                                                        CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                  CELLULAR AMINOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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N-LINKED
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N-LINKED
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GNRH2.
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100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                        369
                                                                                                                                            2017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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2038
2811
3033
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NP_BIND
SITE
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CARBOHYD
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INIT_MET
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GONZ_HAPBU
ID P37044
AC P37044
DT 01-JUN
DT 30-MAX
DE GORBO-
DE GORBO-
CO CORPO-
CO ACTINC
OC AC
                               CHAIN
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002012; ...
Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GONADOLIBERIN II.
GONRA-ASSOCIATED PEPTIDE II-1 (POTENTIAL)
GONRA-ASSOCIATED PEPTIDE II-2 (POTENTIAL)
PYRROLIDONE CARBOXVLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holland M.C.H., Gothilf Y., Meiri I., King J.A., Okuzawa K.,
Elizur A., Zohar Y.,
"Levels of the native forms of GnRH in the pituitary of the gilthead
seabream, Sparus aurata, at several characteristic stages of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GONADOLIBERIN II PRECURSOR (GONADOTROPIN-RELEASING HORMONE II)
GONATOLIA MELAZOA: CHORDAR Sea bream).
Sparus aurata (Gilthead sea bream).
BUMARYOTA: MetaZOA: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Sparus.
Sparidae; Sparus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION (G-34 PROVIDE AMIDE GROUP). CF8C0EDBF277365F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Powell J.F.F., Zohar Y., Elizur A., Park M., Fischer W.H.,
Craig A.G., Rivier J.E., Lovejoy D.A., Sherwood N.M.;
"Three forms of gonadotropin-releasing hormone characterized from
TISSUE SPECIFICITY: EXPRESSED IN ONLY ONE CELL GROUP IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).

-i- FUNCTION: STIMULATE THE SECRETION OF GONADOTROPINS.

-i- MASS SPECTROMENTRY: MW=1236.6; METHOD-MALDI; RANGE=24-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROGONADOLIBERIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 1;
Pred. No. 9.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AA.
                                                    -!- SIMILARITY: BELONGS TO THE GNRH FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comp. Endocrinol. 112:394-405(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=99061849; PubMed=9843645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95083645; PubMed=7991588;
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100.08; Liv
                                                                                                                                                                                                                                                                                                                      EMBL; L27435; AAA74993.1; -.
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85
33
64
85
24
33
9631 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                           MESENCEPHALON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8175;
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SEQUENCE
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CC This SWISS-PROT entry: BELONGS TO THE GNRH FAMILY.

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CC or send an email to license@isb-sib.ch).

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Length 85; 0; Indels

Query Match 2.0%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 9.8; Matches 7; Conservative 0; Mismatches

2 LLLGLLL 8 |||||||| 8 LLLGLLL 14

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Search completed: September 5, 2001, 10:58:05 Job time: 117 sec Q68816 hepatitis case of 16748 homo sapien ol6746 homo sapien ol6742 homo sapien ol6742 homo sapien ol6741 homo sapien ol6741 homo sapien ol9927 hepatitis cospano ol68801 hepatitis cospano ol68801 hepatitis cospano ol690401 cavia (guin ol990401 cavia (guin ol990401 cavia (guin ol900401 cavia cavia cavia ol900401 cavia c

9 2.6 364 14 Q68816 9 2.6 371 4 Q16748 9 2.6 371 4 Q16746 9 2.6 495 4 Q16749	016742 016741 016874 039927 092529	9 2.6 3019 14 Q68801 8 2.3 31 11 Q9QVA5 8 2.3 33 11 Q9QVVI 8 2.3 41 11 Q9QUY1 8 2.3 86 4 Q9H2W9	8 2.3 94 4 Q912W8 8 2.3 116 10 P93284 8 2.3 221 2 Q8KU56 8 2.3 241 11 Q92135	8 2.3 269 10 P93641 P9364 8 2.3 290 10 Q9XH03 Q9Xh0 8 2.3 347 8 Q9MGJ0 Q9mgj0	8 2.3 350 4 Q9H2D3 8 2.3 364 14 009533 8 2.3 364 14 068792 8 2.3 364 14 068807	**10000	SUL 2Y7	DE FALLOTERN.  OS Mus musculus (Mouse).  OC EURaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  OX NCBI_TAXID=10090;  RN [1]	RP SEQUENCE FROM N.A.  RC TISSUE-OVARY;  RA TSai YJ., Lee R.KK., Chen YH., Lin SP., Cheng W.TK.;  RT "CDNA cloning of fallotein from mouse ovary.";  RI RI "Annitted (IAN-1999) to the FMRI./GenRank/DDRI databases.	EMBL; AF117608; AAF22516.1; InterPro; IPR000072; InterPro; IPR000859;			Query Match 100.0%; Score 345; DB 11; Length 345; Best Local Similarity 100.0%; Pred. No. 0; Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps	QY 1 MILIGILLITSALAGQRTGTRAESNLSSKLQLSSDKEQNGVODPRHERVVTISGNGSIHS 6(	Qy 61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 1	QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 1
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.		1845./43 Million cell updates/sec Title: US-09-457-066-43 Perfect score: 345 Sequence: 1 MLLGLLLLTSALAGQRTGTDVALEHHEECDCVCRGNAGG 345	Scoring table: OLIGO Gapext 60.0	Searched: 425026 seqs, 132305027 residues  Word size: 0	Total number of hits satisfying chosen parameters: 425026 Minimum DB seq length: 0	sey tenyen. ssing: Listir	sp_archea:* sp_archea:* sp_bacteria:* sp_fungi:* sp_human:*	9: sp_phate:* 10: sp_phate:* 11: sp_rodent:* 12: sp_unclassified:* 14: sp_virus:*	å th	\$ Query	Score Match Length DB ID	102 29.6 345 11 09JRV3 09JRV8 09JRV8 79 22.9 345 11 09JRV8 09JRV8 09GGV6 57 15 17 345 11 00JRCV6 09GGV6 09GGV6 57 15 17 00JRT20	Q90RA1 Q91946 gallus gal Q101946 gallus gal Q16755 Q16755 homo sapien Q16755 homo sapien Q16755 homo sapien Q Q68809 pepatitis	9 2.6 364 14 Q96851 Q96851 hepatitis 1 9 2.6 364 14 Q96855 Q96855 hepatitis 2 9 2.6 364 14 Q96857 Q96857 hepatitis 2 9 2.6 364 14 Q96857 Q96857 hepatitis	9 2.6 364 14 9 2.6 364 14 9 2.6 364 14 9 2.6 364 14	9 2.6 364 14 Q68800 Q68800 hepatitis 9 2.6 364 14 Q68803 Q68803 hepatitis 9 2.6 364 14 Q68812 Q68812 hepatitis

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                                                              241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECOCVPRK 300
                                                                          SEQUENCE FROM N.A. STRAIN=SWISS-WEBSTER/NIH; STRAIN=SWISS-WEBSTER/NIH; Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.; "The mouse Pdgfc gene: Dynamic expression in embryonic tissues during
GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 TVPGKQTSKGNHIRIRERFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSSLSLDLLN 187
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                    301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FA1486BED6D362F8 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
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Last annotation update)
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Pred. No. 2.9e-91;
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PROSITE; PS50278; PDGF_2; 1.
SMART; SM00042; CUB; 1.
SEQUENCE 345 AA; 38886 MW
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EMBL; AF286725; AAF91483.1;
InterPro; IPR000072; -.
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                                                                                                                                                                                  PRELIMINARY;
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Best Local Similarity.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                     236 VNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQ 295
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=UTERUS;
Tsai Y.J., Lee R.K.K., Lin S.P.;
"Fallotein, a novel growth factor like gene identified in human
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                                                                                                                                                                                              Score 79; DB 11; Length 345;
Pred. No. 8.6e-69;
0; Mismatches 0; Indels
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40. 2.1e-42; Indels
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                                              SCDGF/PDGF-C/fallótein.";
Biochem. Biophys. Res. Commun. 0:0-0(2000).
EMBL, AB033830; BAB199691; -
EMBL, AB038330; BAB199691; -
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100.0%; Pre
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SEQUENCE 345 AA; 39029 MW;
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PROSITE; PS50278; PDGF_2; 1.
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Best Local Similarity 100.
Matches 79; Conservative
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Best Local Similarity 100.
Matches 52; Conservative
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InterPro; IPR000859; -.
Pfam; PF00341; PDGF; 1.
Pfam; PF00431; CUB; 1.
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Q9NRA1

SO DE RESTRETAR DE LA PERSONA DE LA PERSONA

Q9NRA1

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SEQUENCE FROM N.A.

TISSUE-PERIPHERAL BLOOD;

MEDLINE=93024490; PubMed=1406709;

MEDLINE=93024490; PubMed=1406709;

MEDLINE=93024490; PubMed=10, Tabarelli M., Kofler R., White P.C.;

R339H and P453S: CYP21 mutations associated with nonclassic steroid
21-hydroxylase deficiency that are not apparent gene conversions.";

Mol. Endocrinol. 6:1318-1322(1992).

-! CATALYTIC ACTIVITY: A STEROID + AH(2) + O(2) = A 21-HYDROXYSTEROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,
Lesmana L.A., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Jakarta, Indonesia classifiable into
novel genotypes in the second (2e and 2f), tenth (10a) and eleventh
(11a) genetic groups.";
J. Gen. Virol. 77:293-301(1996).
:- SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE.
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U-MAR-2001 (TIEMBLrel. 16, Last annotation update)
STEROID 21-MONOXYGENASE (EC 1.14.99.10) (STEROID 21-HYDROXYLASE)
(CYTOCHROME P450 XXIA1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            Pred. No. 7.4e-23;
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100.0%; Pred. No. 0.78;
ive 0; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
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100.0%; Pro
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-!- COFACTOR: HEME-THIOLATE.
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Best Local Similarity 100.
Matches 9; Conservative
                                              Conservative
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Q68809
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MEDLINE=20317014; PubMed=10858496;
Hamada T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000)
FEBS Lett. 475:97-102(2000)
InterPro; IPR000072; -.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
"PDGF-C is a novel protease-activated ligand for the PDGF alpha
I receptor.";
IN Nat. Cell Biol. 0.0-0(2000).
R EMBL; AF244813; AAP80597.1; -.
R InterPro; IPR00072; -.
R InterPro; IPR000859; -.
R Ffam; PF00431; CUB; 1.
R PROSITE; PS01180; CUB; 1.
R PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590889CEA55CC5EA CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SPINAL CORD-DERIVED GROWTH FACTOR.
GADGE.
Gallus gallus (Chicken).
                                                                       O9DRA1;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
HOMO sapiens (Human).
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                                              PRT;
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PROSITE; PS50278; PDGF_2; 1.
SMART; SM00042; CUB; 1.
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                                              PRELIMINARY;
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SEQUENCE 345 AA; 3
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Q91946 Q91946;

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RESULT Q91946

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SEQUENCE

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Lizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE
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1. GENEL: SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE.
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Hepacivirus.
EMBL; D49768; BAA08602.1; -.
InterPro; IPR002166; -.
Pfam; PF00998; HCV_RGRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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Pfam; PF00998; HCV_RdRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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                                                                                                                                                              2.6%; Score 9; DB 14; Length 364;
100.0%; Pred. No. 2.3;
ive 0; Mismatches 0; Indels
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                                                                                                      74BF8B2BD95964D3 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GENOME POLYPROTEIN (FRAGMENT).
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01-FEB-1997 (TrEMBLrel. 02, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last and
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                                                                                                    364 AA; 40181 MW;
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Best Local Similarity 100.v
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Best Local Similarity
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NCBI_TaxID=11103;
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STRAIN-VN506;
MEDLINE-95062197; PubMed-7972001;
Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tokita H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the
seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
EMBL; D87356; BAA13399.1; -.
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Hepacivirus.
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MEDLINE-95062197;

POKIDA H., OKAMOTO H., TSUDA P., NAKATA S., Chosa T.,

IIZUKA H., MISHIRO S., MIYAKAWA Y., MAYUMI M.;

IIZUKA H., MISHIRO S., MIYAKAWA Y., MAYUMI M.;

"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";

PROC. NALI. RACA SCI. U.S.A. 91:11022-11026(1994).

PLOS. NALIARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE.

EMBL. D87360; BAA13343.1;

INTERPRO: IPRO02166;
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Pfam; PF00998; HCV_RGRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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Submitted (AUG-1996) to the EMBL/GenBank/DDbJ databases.
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Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
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Matches 9; Conservative
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-!- SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE
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NCBI_TaxID=11103;
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 AA; 39910 MW; 139EC77C221080E5 CRC64;
                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GENOME POLYPROTEIN (FRAGMENT).
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-hos 9, Conservative
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                                                           PRELIMINARY;
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Tokita H., Okamoto H., Tizuka H., Kishimoto J., Tsuda F., Lesmana L.A., Miyakawa Y., Mayumi M.; Lesmana L.A., Miyakawa Y., Mayumi M.; "Hepatitis C virus variants from Jakarta, Indonesia classifiable into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups.": Gen. Virol. 77:293-301(1996).
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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InterProx; IPRO02166; -.
Pfam; PF00998; HCV_RARP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
               InterPro; IPR002166; -...
Pfam; PF00998; HCV_RGRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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100.0%; Pred. No. 2.3;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                     Length 364;
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                                                                                                                         364 AA; 39872 MW; C631B44009FBD1C9 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 2.3
Matches 9; Conservative 0; Mismatches
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MEDLINE-96226020; PubMed-8627233;
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EMBL; D87363; BAA13346.1;
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345 LLLGLLLLT 353
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345 LLLGLLLLT 353
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SEQUENCE 364 AA; 40072 MW; 0D7E2B9B49023FBB CRC64;
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